

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 15:03:41 ; Search time 79 Seconds  
(without alignments)  
1552.980 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EFHHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1640122

Minimum DB seq length: 0  
Maximum DB seq length: 342

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1856	100.0	342	3 AAB06205	Immunogen
2	1786	96.2	338	8 ADF90025	Adf90025 Opossum-h
3	1786	96.2	338	8 ADN00646	Adn00646 OSO prote
4	1644.5	88.6	341	3 AAB06208	Aab06208 Immunogen
5	1584.5	85.4	341	3 AAB03644	Aab03644 Opossum I
6	1568.5	84.5	341	3 AAB06206	Aab06206 Immunogen
7	1498.5	80.7	337	8 ADF90022	Adf90022 Opossum-r
8	1498.5	80.7	337	8 ADN00643	Adn00643 OSO prote
9	1392.5	75.0	341	3 AAB06202	Aab06202 Immunogen
10	1375	74.1	342	3 AAB06201	Aab06201 Immunogen
11	1038.5	56.0	320	6 AAO19667	Aao19667 Human IGE
12	1038.5	56.0	323	5 AAU80286	Aau80286 Human IGE
13	1038.5	56.0	323	5 AAU80285	Aau80285 Human IGE
14	1038.5	56.0	323	5 AAU80284	Aau80284 Human IGE
15	1038.5	56.0	324	2 AAR33559	Aar33559 Fc(epsilo
16	1038.5	56.0	325	2 AAR75225	Aar75225 Human IGE
17	1038.5	56.0	325	2 AAR77241	Aar77241 Human IGE
18	1038.5	56.0	331	3 AAB03642	Aab03642 Human IGE
19	1038.5	56.0	331	7 ADD25768	Add25768 Binding d
20	1036.5	55.8	330	5 AAU80289	Aau80289 Human IGE
21	1035.5	55.8	325	3 AAY79994	Aay79994 Human imm
22	1034.5	55.7	326	5 AAU80288	Aau80288 Human IGE
23	1019.5	54.9	335	2 AAR55582	Aar55582 Fc(epsilo
24	1019.5	54.9	325	2 AAR33582	Aar33582 CH2 to CH
25	961	51.8	312	3 AAY79995	Aay79995 Dog immun

26	795.5	42.9	201	2 AAR85589	Aar85589 Fc(epsilo
27	791.5	42.6	220	8 ADL01587	Adl01587 Human mut
28	779.5	42.0	223	8 ADL01584	Adl01584 Human imm
29	778.5	41.9	218	2 AAR85583	Aar85583 Fc(epsilo
30	778.5	41.9	220	8 ADL01589	Adl01589 Human mut
31	778.5	41.9	222	4 ABP60380	Abp60380 Human IGE
32	778.5	41.9	222	4 AAG65599	Aag65599 Amino aci
33	778.5	41.9	222	8 ADL01578	Adl01578 Human imm
34	777.5	41.9	220	8 ADL01593	Adl01593 Human mut
35	777.5	41.9	220	8 ADL01603	Adl01603 Human mut
36	774.5	41.7	220	8 ADL01599	Adl01599 Human mut
37	773.5	41.7	220	8 ADL01601	Adl01601 Human mut
38	773.5	41.7	220	8 ADL01595	Adl01595 Human mut
39	773.5	41.7	220	8 ADL01591	Adl01591 Human mut
40	772.5	41.6	220	8 ADL01597	Adl01597 Human mut
41	767.5	41.4	340	3 AAB03643	Aab03643 Rat IGE h
42	746.5	40.2	332	5 AAU80298	Aau80298 Murine Ig
43	746.5	40.2	332	5 AAU80299	Aau80299 Murine Ig
44	746.5	40.2	332	5 AAU80297	Aau80297 Mouse IGE
45	738.5	39.3	313	3 AAY79996	Aay79996 Rat immun

#### ALIGNMENTS

RESULT 1  
AAB06205  
ID AAB06205 standard; protein; 342 AA.  
XX AAB06205;  
AC AAB06205;  
XX  
DT 12-SEP-2003 (revised)  
DT 22-NOV-2000 (first entry)  
XX  
DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.  
XX Human; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
KW asthma; eczema; immunogenic peptide.  
XX  
OS Didelphis virginiana.  
OS Homo sapiens.  
OS Chimeric.  
XX  
PN WO200025722-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 21-OCT-1999; 99WO-SE001896.  
XX  
PR 02-NOV-1998; 98US-0106652P.  
PR 22-SEP-1999; 99US-00401636.  
XX  
PA (RESI-) RESISTENTIA PHARM AB.  
XX  
PI Hellman LT;  
XX  
DR WPI; 2000-365342/31.  
XX  
PT Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.  
XX  
PS Disclosure; Fig 2; 50pp; English.  
XX  
CC The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the human. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.  
CC (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 342 AA;  
 Query Match 100.0%; Score 1856; DB 3; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-146;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHHHHHHHTLSPESGPVTTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTW 60  
 DB 1 EHHHHHHHTLSPESGPVTTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTW 60

QY 61 LVDGQAEALFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSR 120  
 DB 61 LVDGQAEALFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSR 120

QY 121 KCADSNPRGVSAVLSRPSFDLFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHST 180  
 DB 121 KCADSNPRGVSAVLSRPSFDLFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHST 180

QY 181 RXEEKORNGTLVTSTLPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240  
 DB 181 RXEEKORNGTLVTSTLPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240

QY 241 MLPPSPETGTTRVTCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 300  
 DB 241 MLPPSPETGTTRVTCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 300

QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 2  
 ADF90025  
 ID ADF90025 standard; protein; 338 AA.  
 AC ADF90025;  
 XX  
 XX 26-FEB-2004 (first entry)  
 DT  
 XX Opossum-human chimeric IGE polypeptide.  
 DE IGE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;  
 KW antidiathmatic; dermatological.  
 KW  
 XX Chimeric.  
 OS Didelphis virginiana.  
 OS Homo sapiens.  
 XX  
 PN WO2003096966-A2.  
 XX  
 PD 27-NOV-2003.  
 XX  
 PF 15-MAY-2003; 2003WO-IB002503.  
 XX  
 PR 21-MAY-2002; 2002US-0382552P.  
 XX  
 PA (RESI-) RESISTENTIA PHARM AB.  
 XX  
 XX Lundgren M, Fuentes A, Magnusson A;  
 PI WPI; 2004-042496/04.  
 DR N-PSDB; ADF90024, ADF90023.  
 DR  
 XX New host cell comprising a nucleic acid vector comprising a  
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or  
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IGE  
 PT polypeptide.  
 XX  
 XX Claim 3; SEQ ID NO 6; 23pp; English.  
 PS  
 XX The present sequence is the protein sequence of an opossum CH2-human CH3-  
 CC opossum CH4 (OSO) chimeric IGE polypeptide. A vector comprising DNA  
 CC encoding OSO can be used for recombinant production this chimeric IGE in

CC host, e.g. CHO, cells. The invention provides methods and materials  
 CC related to expressing chimeric IGE proteins. Nucleic acid vectors, host  
 CC cells, and methods for producing chimeric IGE polypeptides are provided.  
 CC When administered to a mammal, the chimeric polypeptides can reduce the  
 CC IGE antibody effects of IGE-related diseases such as asthma, allergies  
 CC and eczema.  
 XX  
 SQ Sequence 338 AA;  
 Query Match 96.2%; Score 1786; DB 8; Length 338;  
 Best Local Similarity 99.4%; Pred. No. 3.6e-140;  
 Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTWLDGQAE 68  
 DB 3 TLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTWLDGQAE 62

QY 69 NLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128  
 DB 63 NLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122

QY 129 GVSAYLSRSPDLPFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKKEKQ 188  
 DB 123 GVSAYLSRSPDLPFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKKEKQ 182

QY 189 GTLTVTSTLPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKL - PGKRLAPEVYMLPPSP 246  
 DB 183 GTLTVTSTLPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKLASPGKRLAPEVYMLPPSP 242

QY 247 EETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFLSRMLV 306  
 DB 243 EETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFLSRMLV 302

QY 307 NKSIMEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 303 NKSIMEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 3  
 ADF90025  
 ID ADF90025 standard; protein; 338 AA.  
 AC ADF90025;  
 XX  
 XX 17-JUN-2004 (first entry)  
 DT  
 XX OSO protein, SEQ ID 6.  
 DE  
 XX Antiallergic; Vaccine; self-IgE; OSO; allergy.  
 KW  
 XX Synthetic.  
 OS  
 XX WO2004022094-A1.  
 PN  
 XX 18-MAR-2004.  
 PD  
 XX 02-JUN-2003; 2003WO-IB003075.  
 PF  
 XX 05-SEP-2002; 2002US-0408648P.  
 PR  
 XX (RESI-) RESISTENTIA PHARM AB.  
 PA  
 XX Hellman LT, Persson S, Gansson A;  
 PI WPI; 2004-248376/23.  
 DR N-PSDB; ADF90024.  
 DR  
 XX New composition comprising a self-IgE polypeptide and an aluminum  
 PT compound, useful for inducing an anti self-IgE antibody response in a  
 PT mammal for treating or preventing allergies.  
 XX  
 XX Claim 3; Fig 8; 102pp; English.  
 PS  
 XX

CC The present invention relates to a composition comprising a polypeptide  
CC and an aluminum compound, where the polypeptide comprises a self-IgE  
CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;  
CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or  
CC ADN00661). Administration of the composition to a mammal reduces the  
CC level of detectable free IgE in the mammal. The composition is useful for  
CC inducing an anti self-IgE antibody response in a mammal for treating or  
CC preventing allergies. The present sequence is an OSO protein, used to  
CC illustrate the invention. The OSO protein contains an opossum CH2 IgE  
CC domain followed by a human CH3 IgE domain followed by an opossum CH4 IgE  
CC domain.  
XX  
SQ Sequence 338 AA;

Query Match 96.2%; Score 1786; DB 8; Length 338;  
Best Local Similarity 99.4%; Pred. No. 3 6e-140; Indels 2; Gaps 1;  
Matches 334; Conservative 0; Mismatches 0; Mismatches 0; Indels 2; Gaps 1;  
QY 9 TISLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVDQAE 68  
Db 3 TISLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVDQAE 62  
QY 69 NUPPYTRRKREGGQTFSLQSEVNIITOGWMSNTYTCHVKNGSTIFEDSSRKADSNPR 128  
Db 63 NUPPYTRRKREGGQTFSLQSEVNIITOGWMSNTYTCHVKNGSTIFEDSSRKADSNPR 122  
QY 129 GVSAYLSRSPSPDLFIRKSPPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKQRN 188  
Db 123 GVSAYLSRSPSPDLFIRKSPPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKQRN 182  
QY 189 GILVTSTLPVGTQWIEGETYQCRVTHPHLPRALMRSTTKL--PGKRLAPEVYMLPSP 246  
Db 183 GILVTSTLPVGTQWIEGETYQCRVTHPHLPRALMRSTTKLASPGKRLAPEVYMLPSP 242  
QY 247 EETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLLYRMLV 306  
Db 243 EETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLLYRMLV 302  
QY 307 NKSIVKGNLVTQVHVEALPGSRTLEKSLHYSAGN 342  
Db 303 NKSIVKGNLVTQVHVEALPGSRTLEKSLHYSAGN 338

RESULT 4  
AAB06208  
ID AAB06208 standard; protein; 341 AA.  
XX  
AC AAB06208;  
XX  
DT 12-SEP-2003 (revised)  
DT 22-NOV-2000 (first entry)  
XX  
DE Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.  
XX  
KW Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
KW asthma; eczema; immunogenic peptide.  
XX  
OS Didelphis virginiana.  
OS Canis sp.  
OS Chimeric.  
XX  
PN WO2000025722-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 21-OCT-1999; 99WO-SE001896.  
XX  
PR 02-NOV-1998; 98US-0106652P.  
PR 22-SEP-1999; 99US-00401636.  
XX  
PA (RESI-) RESISTENTIA PHARM AB.  
XX  
PI Hellman LT;

XX WPI; 2000-365342/31.  
DR  
XX Immunogenic polypeptides useful for preventing the harmful effects of  
XX immunoglobulin E in mammals.  
PT  
PS Disclosure; Fig 2; 50pp; English.  
XX  
CC The present sequence is an immunogenic peptide consisting of the heavy  
CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain  
CC constant region 3 from the dog. It was shown to cause a stronger  
CC polyclonal anti-self IgE response than peptides consisting of the same  
CC regions from one mammal. Immunogenic peptides, particularly those  
CC consisting of different heavy chain constant regions, can be used for  
CC vaccination in humans, against bacterial and viral infections and  
CC allergies, such as asthma, fur, pollen and food allergies and eczema.  
CC (Updated on 12-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 341 AA;

Query Match 88.6%; Score 1644.5; DB 3; Length 341;  
Best Local Similarity 88.0%; Pred. No. 2.2e-128; Indels 1; Gaps 1;  
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;  
QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60  
Db 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60  
QY 61 LVDQAEANLFPYTRRKREGGQTFSLQSEVNIITOGWMSNTYTCHVKNGSTIFEDSSR 120  
Db 61 LVDQAEANLFPYTRRKREGGQTFSLQSEVNIITOGWMSNTYTCHVKNGSTIFEDSSR 120  
QY 121 KCADSNRPGVSAYLSRSPSPDLFIRKSPPTITCLVVDLAPSKGTVNLTWASRASKPVNHS 180  
Db 121 KCESDPRGVTSLSPSPDLVYHKAPKITCLVVDLATWEG-MNLTWYRESKEPVNPGP 179  
QY 181 RKEKQKNGTLTSTLPVGTQWIEGETYQCRVTHPHLPRALMRSTTKLPKELAPEVY 240  
Db 180 LNKDHFNGTITVSTLPVNTDWEGETYTCRVTHPHLPDILVRSIAKLPKELAPEVY 239  
QY 241 MLPPSPETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLL 300  
Db 240 MLPPSPETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLL 299  
QY 301 YSRMLVKSIVKGNLVTQVHVEALPGSRTLEKSLHYSAGN 342  
Db 300 YSRMLVKSIVKGNLVTQVHVEALPGSRTLEKSLHYSAGN 341

RESULT 5  
AAB03644  
ID AAB03644 standard; protein; 341 AA.  
XX  
AC AAB03644;  
XX  
DT 22-NOV-2000 (first entry)  
XX  
DE Opossum IgE heavy chain constant regions 2, 3 and 4.  
XX  
KW Opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma;  
KW eczema; immunogenic peptide.  
XX  
OS Didelphis virginiana.  
XX  
PN WO2000025722-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 21-OCT-1999; 99WO-SE001896.  
XX  
PR 02-NOV-1998; 98US-0106652P.  
PR 22-SEP-1999; 99US-00401636.  
XX  
XX

PA (RESI-) RESISTENTIA PHARM AB.  
 XX Hellman LT;  
 PI WPI; 2000-365342/31.  
 DR  
 XX Immunogenic polypeptides useful for preventing the harmful effects of  
 PT immunoglobulin E in mammals.  
 PT  
 XX Disclosure; Fig 1; 50pp; English.  
 PS  
 XX The present sequence is an immunogenic peptide consisting of the heavy  
 CC chain constant regions 2, 3 and 4 of the opossum IgE. It was used to  
 CC construct a number of immunogenic peptides which consisted of regions of  
 CC IgE from different mammals, which appear to cause a stronger polyclonal  
 CC anti-self IgE response than peptides consisting of the same regions from  
 CC one mammal. Immunogenic peptides, particularly those consisting of  
 CC different heavy chain constant regions, can be used for vaccination in  
 CC humans, against bacterial and viral infections and allergies, such as  
 CC asthma, fur, pollen and food allergies and eczema  
 CC  
 XX Sequence 341 AA;  
 SQ  
 Query Match 85.4%; Score 1584.5; DB 3; Length 341;  
 Best Local Similarity 85.1%; Pred. No. 2.2e-123;  
 Matches 291; Conservative 22; Mismatches 28; Indels 1; Gaps 1;  
 QY 1 EFHHHHHTLSLSPESGPTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 DB 1 EFHHHHHTLSLSPESGPTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 QY 61 LVDQQAENLFPVYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120  
 DB 61 LVDQQAENLFPVYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSAQ 120  
 QY 121 KCADSNPRGSAVLSRSPDFIRKSPITCLVLDLAPSKGTVNLTPWRSAGKPVNHST 180  
 DB 121 KCSDTOPRGISAVILPPTQDLFVKKVTIGCLIVDLA-SAENVKVTWRSRSGGPNPSS 179  
 QY 181 RKEKQNGRLTVTSTLPVGTDRWIEGTYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 240  
 DB 180 LVKEQNGRLTVTSTLPVGTDRWIEGTYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 239  
 QY 241 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 300  
 DB 240 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 299  
 QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341  
 RESULT 6  
 AAB06206  
 ID AAB06206 standard; protein; 341 AA.  
 XX AAB06206;  
 AC  
 XX  
 XX 12-SEP-2003 (revised)  
 DT 22-NOV-2000 (first entry)  
 XX  
 XX Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.  
 XX Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
 KW asthma; eczema; immunogenic peptide.  
 XX  
 XX Didelphis virginiana.  
 OS Rattus sp.  
 OS Chimeric.  
 XX WO200025722-A2.  
 FN  
 XX 11-MAY-2000.  
 PD

XX 21-OCT-1999; 99WO-SE001896.  
 PF  
 XX 02-NOV-1998; 98US-0106652P.  
 PR  
 XX 22-SEP-1999; 99US-00401636.  
 XX  
 XX (RESI-) RESISTENTIA PHARM AB.  
 PA  
 XX Hellman LT;  
 PI WPI; 2000-365342/31.  
 DR  
 XX Immunogenic polypeptides useful for preventing the harmful effects of  
 PT immunoglobulin E in mammals.  
 PT  
 XX Disclosure; Fig 2; 50pp; English.  
 PS  
 XX The present sequence is an immunogenic peptide consisting of the heavy  
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain  
 CC constant region 3 from the rat. It was shown to cause a stronger  
 CC polyclonal anti-self IgE response than peptides consisting of the same  
 CC regions from one mammal. Immunogenic peptides, particularly those  
 CC consisting of different heavy chain constant regions, can be used for  
 CC vaccination in humans, against bacterial and viral infections and  
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.  
 CC (Updated on 12-SEP-2003 to standardise OS field)  
 CC  
 XX Sequence 341 AA;  
 SQ  
 Query Match 84.5%; Score 1568.5; DB 3; Length 341;  
 Best Local Similarity 83.3%; Pred. No. 4.6e-122;  
 Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;  
 QY 1 EFHHHHHTLSLSPESGPTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 DB 1 EFHHHHHTLSLSPESGPTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 QY 61 LVDQQAENLFPVYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120  
 DB 61 LVDQQAENLFPVYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120  
 QY 121 KCADSNPRGSAVLSRSPDFIRKSPITCLVLDLAPSKGTVNLTPWRSAGKPVNHST 180  
 DB 121 RCDSDPRGVITLIPSPDLGYENGTPKLTCLVLDL-ESEENITVTVWRKKSIGSAS 179  
 QY 181 RKEKQNGRLTVTSTLPVGTDRWIEGTYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 240  
 DB 180 QRSTKHNATTSITSLPVDKADWIEGTYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 239  
 QY 241 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 300  
 DB 240 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 299  
 QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341  
 RESULT 7  
 ADF90022  
 ID ADF90022 standard; protein; 337 AA.  
 XX ADF90022;  
 AC  
 XX 26-FEB-2004 (first entry)  
 DT  
 XX Opossum-rat chimeric IgE polypeptide.  
 DE  
 XX IgE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;  
 KW antiasthmatic; dermatological.  
 XX Chimeric.  
 OS Didelphis virginiana.  
 OS



```

OS Rattus sp.
XX WO2003096966-A2.
XX 27-NOV-2003.
XX 15-MAY-2003; 2003WO-IB002503.
XX 21-MAY-2002; 2002US-0382552P.
XX (RESI-) RESISTENTIA PHARM AB.
XX Lundgren M, Fuentes A, Magnusson A;
XX WPI; 2004-042496/04.
XX N-PSDB; ADF90020, ADF90021.
XX New host cell comprising a nucleic acid vector comprising a
XX cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
XX SV40 late polyadenylation sequence, useful in producing a chimeric IgE
XX polypeptide.
XX Claim 3; SEQ ID NO 3; 23pp; English.
XX The present sequence is the protein sequence of an opossum CH2-rat CH3-
XX opoosum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic
XX acid encoding ORO can be used for recombinant production of this chimeric
XX IgE in host, e.g. CHO, cells. The invention provides methods and
XX materials related to expressing chimeric IgE proteins. Nucleic acid
XX vectors, host cells, and methods for producing chimeric IgE polypeptides
XX are provided. When administered to a mammal, the chimeric polypeptides
XX can reduce the IgE antibody effects of IgE-related diseases such as
XX asthma, allergies and eczema.
XX SQ Sequence 337 AA;
Query Match 80.7%; Score 1498.5; DB 8; Length 337;
Best Local Similarity 82.4%; Pred. No. 3.1e-116;
Matches 277; Conservative 20; Mismatches 36; Indels 3; Gaps 2;
QY 9 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLFPTTRPKREGGQTFSLQSEVNITQGMWSSNTYTCHVKNGSIFEDSSRRCDSNPR 128
DB 63 NLFPTTRPKREGGQTFSLQSEVNITQGMWSSNTYTCHVKNGSIFEDSSRRCDSNPR 122
QY 129 GVSAYLSRSPFDLFIKSPFTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEKORN 188
DB 123 GVITTLIPSPDLIYENGTPKLTCLVLDL-ESEENITVTVRERKKSIGASQSTKHNN 181
QY 189 GTLTVTSTLPVGRDWIEGETYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 182 ATTSITSLPVDKADWIEGEGYQCRVDHPHFKPIVRSITKLASPGKRLAPEVYMLPPSP 241
QY 247 EETGTRTITVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 306
DB 242 EETGTRTITVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 301
QY 307 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 302 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 337
RESULT 8
ADN00643
ID ADN00643 standard; protein; 337 AA.
XX AC ADN00643;
XX DT 17-JUN-2004 (first entry)
XX

```

```

DE ORO protein, SEQ ID 3.
XX Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
XX OS Synthetic.
XX WO2004022094-A1.
XX 18-MAR-2004.
XX 02-JUN-2003; 2003WO-IB003075.
XX 05-SEP-2002; 2002US-0408648P.
XX (RESI-) RESISTENTIA PHARM AB.
XX Hellman LT, Persson S, Ganssion A;
XX WPI; 2004-248376/23.
XX N-PSDB; ADN00642.
XX New composition comprising a self-IgE polypeptide and an aluminum
XX compound, useful for inducing an anti self-IgE antibody response in a
XX mammal for treating or preventing allergies.
XX Claim 3; Fig 4; 102pp; English.
XX The present invention relates to a composition comprising a polypeptide
XX and an aluminum compound, where the polypeptide comprises a self-IgE
XX polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide:
XX ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
XX ADN00661). Administration of the composition to a mammal reduces the
XX level of detectable free IgE in the mammal. The composition is useful for
XX inducing an anti self-IgE antibody response in a mammal for treating or
XX preventing allergies. The present sequence is an ORO protein, used to
XX illustrate the invention. The ORO protein contains an opoosum CH2 IgE
XX domain followed by a rat CH3 IgE domain followed by an opoosum CH4 IgE
XX domain.
XX SQ Sequence 337 AA;
Query Match 80.7%; Score 1498.5; DB 8; Length 337;
Best Local Similarity 82.4%; Pred. No. 3.1e-116;
Matches 277; Conservative 20; Mismatches 36; Indels 3; Gaps 2;
QY 9 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLFPTTRPKREGGQTFSLQSEVNITQGMWSSNTYTCHVKNGSIFEDSSRRCDSNPR 128
DB 63 NLFPTTRPKREGGQTFSLQSEVNITQGMWSSNTYTCHVKNGSIFEDSSRRCDSNPR 122
QY 129 GVSAYLSRSPFDLFIKSPFTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEKORN 188
DB 123 GVITTLIPSPDLIYENGTPKLTCLVLDL-ESEENITVTVRERKKSIGASQSTKHNN 181
QY 189 GTLTVTSTLPVGRDWIEGETYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 182 ATTSITSLPVDKADWIEGEGYQCRVDHPHFKPIVRSITKLASPGKRLAPEVYMLPPSP 241
QY 247 EETGTRTITVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 306
DB 242 EETGTRTITVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 301
QY 307 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 302 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 337
RESULT 9
AAB06202
ID AAB06202 standard; protein; 341 AA.

```

XX AC AAB06202;  
 XX DT 12-SEP-2003 (revised)  
 XX DT 22-NOV-2000 (first entry)  
 XX DE Immunogenic peptide consisting of opossum CH2, mouse CH3 and opossum CH4.  
 XX KW Mouse; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
 XX KW asthma; eczema; immunogenic peptide.  
 XX OS Didelphis virginiana.  
 XX OS Mus sp.  
 XX OS Chimeric.  
 XX FH Key Location/Qualifiers  
 XX FT Misc-difference 1..341  
 XX FT /label= OTHER  
 XX FT /note= "Xaa=unknown"  
 XX PN WO200025722-A2.  
 XX PD 11-MAY-2000.  
 XX PF 21-OCT-1999; 99WO-SE001896.  
 XX PR 02-NOV-1998; 98US-0106652P.  
 XX PR 22-SEP-1999; 99US-00401636.  
 XX PA (RESI-) RESISTENTIA PHARM AB.  
 XX PI Hellman LT;  
 XX DR WPI; 2000-365342/31.  
 XX XX Immunogenic polypeptides useful for preventing the harmful effects of  
 XX immunoglobulin E in mammals.  
 XX PS Disclosure; Fig 2; 50pp; English.  
 XX CC The present sequence is an immunogenic peptide consisting of the heavy  
 XX chain constant regions 2 and 4 of the opossum IGE and the heavy chain  
 XX constant region 3 from the mouse. It was shown to cause a stronger  
 XX polyclonal anti-self IgE response than peptides consisting of the same  
 XX regions from one mammal. Immunogenic peptides, particularly those  
 XX consisting of different heavy chain constant regions, can be used for  
 XX vaccination in humans, against bacterial and viral infections and  
 XX allergies, such as asthma, fur, pollen and food allergies and eczema.  
 XX CC (Updated on 12-SEP-2003 to standardise OS field)  
 XX SQ Sequence 341 AA;  
 Query Match 75.0%; Score 1392.5; DB 3; Length 341;  
 Best Local Similarity 76.8%; Pred. No. 2.le-107;  
 Matches 263; Conservative 22; Mismatches 53; Indels 5; Gaps 3;  
 QY 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 DB 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 QY 61 LVDGQAEHLFPYTTTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120  
 DB 61 LVDGQAEHLFPYTTTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAVLSRPSFDFIRKSPITCLVWDLAPSKGTVALTWSRASKPVNHS 180  
 DB 121 RCPDEPRGVITVILPSPDLJYQHCAKPLTCLVLDLSEK-HINVTWNQ--KPTXXA 177  
 QY 181 RK--EKQKNGTLVTSTLPVGTROMIEGETYOCRTVHPALMRSTTKLPGRKLAPE 238  
 DB 178 XOWYTKHHHAHTXTISILPVVXKDWIEGYXQIXDHPHPKIXXVPSITRPLGKRLAPX 237  
 QY 239 VYMLPPSPETGTRTTRVTCILRGFYSEISVQWLFNNEEDHTGHTTTRPQKHGDTXSF 298

DB 238 VYMLPPSPETGTRTTRVTCILRGFYSEISVQWLFNNEEDHTGHTTTRPQKHGDTXSF 297  
 QY 299 FLYSRLMLVKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 341  
 DB 298 FLYSRLMLVKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340  
 RESULT 10  
 AAB06201  
 ID AAB06201 standard; protein; 342 AA.  
 XX AC AAB06201;  
 XX DT 12-SEP-2003 (revised)  
 XX DT 22-NOV-2000 (first entry)  
 XX DE Immunogenic peptide consisting of opossum CH2, CH4 and rat/opossum CH3.  
 XX KW Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
 XX KW asthma; eczema; immunogenic peptide.  
 XX OS Didelphis virginiana.  
 XX OS Rattus sp.  
 XX OS Chimeric.  
 XX FH Key Location/Qualifiers  
 XX FT Misc-difference 1..342  
 XX FT /label= OTHER  
 XX FT /note= "Xaa=unknown"  
 XX PN WO200025722-A2.  
 XX PD 11-MAY-2000.  
 XX PF 21-OCT-1999; 99WO-SE001896.  
 XX PR 02-NOV-1998; 98US-0106652P.  
 XX PR 22-SEP-1999; 99US-00401636.  
 XX PA (RESI-) RESISTENTIA PHARM AB.  
 XX PI Hellman LT;  
 XX DR WPI; 2000-365342/31.  
 XX XX Immunogenic polypeptides useful for preventing the harmful effects of  
 XX immunoglobulin E in mammals.  
 XX PS Disclosure; Fig 2; 50pp; English.  
 XX CC The present sequence is an immunogenic peptide consisting of the heavy  
 XX chain constant regions 2 and 4 of the opossum IGE and the heavy chain  
 XX constant region 3 created from a combination of the one from the rat and  
 XX the one from the opossum. It was shown to cause a stronger polyclonal  
 XX anti-self IgE response than peptides consisting of the same regions from  
 XX one mammal. Immunogenic peptides, particularly those consisting of  
 XX different heavy chain constant regions, can be used for vaccination in  
 XX humans, against bacterial and viral infections and allergies, such as  
 XX asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-  
 XX 2003 to standardise OS field)  
 XX SQ Sequence 342 AA;  
 Query Match 74.1%; Score 1375; DB 3; Length 342;  
 Best Local Similarity 76.8%; Pred. No. 6e-106;  
 Matches 262; Conservative 23; Mismatches 55; Indels 2; Gaps 2;  
 QY 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 DB 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 QY 61 LVDGQAEHLFPYTTTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120

Db 61 LVDDQAEHLFPYTRPKREGGCTSLQSEVHITQGHSSHTYCHVKXXGSIFFDSR 120  
 Qy 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHST 180  
 Db 121 RUCSDPRGVITVLPSPDLJEHGTGPKLTCLVLDL-ESEEHIXVTWVXRPKXIGAR 179  
 Qy 181 RKEEKOR-NGTLTVTSTLPGVTRDWTIEGTYQCRVTHPLPALMRSTTKLPGRKLAPEV 239  
 Db 180 SLVVKEXYHGTFTXTSHLPVETDDMTGXTYTXLESPPMIVILPTI-SALPGKELAPV 239  
 Qy 240 YMLPPSPETGTRVTVTCIRGYPSEISVQWLFNNEEDHTGHHTTTPQKHGTDPGFF 299  
 Db 240 YMLPPSPETGTRVTVTCIRGYPSEISVQWLFNNEEDHTGHHTTTPQKHGTDPGFF 299  
 Qy 300 LYSRMLVNKSIWEKGNLTVCRVVHEALPGSRILEKSLHYSAG 341  
 Db 300 LYSRMLVNKSIWEKGNLTVCRVVHEALPGSRILEKSLHYSAG 341

## RESULT 11

AAO19667

ID AAO19667 standard; protein; 320 AA.

XX

AC AAO19667;

XX

DT 28-MAR-2003 (first entry)

XX

DE Human IgE heavy chain constant region CH2-CH3-CH4 portion.

XX

KW Human; IgE; immunoglobulin E; immunotherapy; immune disease;

KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;

KW antiasthmatic; antiallergic; antinflammatory; dermatological;

KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;

KW CH2-CH3-CH4 region.

XX

OS Homo sapiens.

XX

XX WO20028317-A2.

XX

PD 07-NOV-2002.

XX

PF 01-MAY-2002; 2002WO-US013527.

XX

PR 01-MAY-2001; 2001US-00847208.

XX

PR 24-OCT-2001; 2001US-00000439.

XX

PA (REGC) UNIV CALIFORNIA.

XX

XX Saxon A, Zhang X, Zhu D;

XX

XX WPI; 2003-103456/09.

XX

PS Claim 21; Fig 6; 116pp; English.

XX The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (Fc epsilon R). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of,

CC or symptoms resulting from, a type I hypersensitivity reaction in a  
 CC subject receiving immunotherapy. The present sequence is the human IgE  
 CC heavy chain constant region CH2-CH3-CH4 portion

XX Sequence 320 AA;

Query Match 56.0%; Score 1038.5; DB 6; Length 320;  
 Best Local Similarity 62.4%; Pred. No. 5.7e-78;  
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

Qy 22 PPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKVHVTLVDCQEAENLFPYTRPKREG 81  
 Db 3 PPTVKILQSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTQE 60  
 Qy 82 GQTFLOSQVNIITQGMSSNTYTCVYKHNGSIFEDSSRKCADSNPRGVSAYLSRSPFD 141  
 Db 61 GELASTQSELTLSQKWLSDRYTCQVYQGHITFEDSTKCADSNPRGVSAYLSRSPFD 120  
 Qy 142 LFRKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTKKEKQNGTLTVTSTLPVGT 201  
 Db 121 LFRKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTKKEKQNGTLTVTSTLPVGT 180  
 Qy 202 RDIWEGTYQCRVTHPLPALMRSTTKLPKSLAPEVYMLPPSPETGT--TRTVTCLI 259  
 Db 181 RDIWEGTYQCRVTHPLPALMRSTTKSGPAADEVYAF-ATPEWFGSRDKRTLACLI 239  
 Qy 260 RGFYPSISVQWLFNNEEDHTGHHTTTPQKHGTDPSPFFLYSRMLVNKSIWEKGNLVC 319  
 Db 240 QNFMPEDISVQWLFNNEEDHTGHHTTTPQKHGTDPSPFFLYSRMLVNKSIWEKGNLVC 297  
 Qy 320 RVVHEALPGSRILEKSLHYSAG 341  
 Db 298 RAVHEAASPSTVORAVSVNPG 319

## RESULT 12

AAU80286

ID AAU80286 standard; protein; 323 AA.

XX

AC AAU80286;

XX

DT 30-JUL-2002 (first entry)

XX

DE Human IgE C2-C3-C4 domains for E.Coli expression.

XX

XX IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
 XX antiasthmatic; dermatological; antinflammatory; immunoglobulin E; IgE;  
 XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
 XX heavy chain C domain.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

XX WO200220038-A2.

XX

XX 14-MAR-2002.

XX

XX 06-SEP-2001; 2001WO-DK000579.

XX

XX 06-SEP-2000; 2000DK-00001326.

XX

XX 15-SEP-2000; 2000US-0232831P.

XX

XX (PHAR-) PHARMEXA AS.

XX

XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;

XX

XX WPI; 2002-383033/41.

XX

XX N-PSDB; ABK51134.

XX

XX Inducing immune response against autologous immunoglobulin E in an  
 XX animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
 XX epitope an/or B-cell epitope derived from the immunoglobulin.

XX

```

PS Disclosure; Page 112-113; 151pp; English.
XX
CC This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (IgE) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes of
CC the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response against
CC autologous IgE in an animal, which is useful for downregulating
CC autologous IgE in the animal. This method is useful in the prevention and
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC asthma and atopic dermatitis. The present sequence represents the human
CC IgE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli
CC system, this sequence was used to create the epitopes of the invention
XX
SQ Sequence 323 AA;

Query Match          56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTWLDGQEAENLFPVYTRPKREG 81
DB 6 PPTVKILQSCDGGHFPPTIQLCLVSGYTGCTINITWLDGQVMD--VDLSTASTTQE 63

QY 82 GQTFSLQSEVNIQTGOWMSNTYTCHVKNGSIFEDSSRKCADSNPRGVSAVLSRPSF 141
DB 64 GELASTQSELTLSQKHLSDRTYTCQVYQGHTEFDSSTKCADSNPRGVSAVLSRPSF 123

QY 142 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 201
DB 124 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 183

QY 202 RWDIEGTYQCRVTHPHLPRALMRSTTKLPKRLAPEVYMLPSPSETGT--TRVTCL 259
DB 184 RWDIEGTYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF--ATPEWFGSRDKRTLACLI 242

QY 260 RGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLVNSIWEKGNLVC 319
DB 243 QNFMPEDISVQWLNHEVQLPDARHSTTPRKTKGS--GFVFSRLVETRAEWEQKDEFIC 300

QY 320 RVVHEALPGSRTLEKSLHYSAG 341
DB 301 RAVHEAASPQTQVRAVSNPG 322

RESULT 13
AAU80285
XX AAU80285 standard; protein; 323 AA.
XX
XX AAU80285;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human IgE C2-C3-C4 domains for mammalian expression.
XX
XX IgE; allergic; human; antiallergic; immunosuppressive; antianaphylactic;
XX antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
XX heavy chain C domain.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO200220038-A2.
XX
XX 14-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-DK000579.
XX
XX 06-SEP-2000; 2000DK-00001326.

```

---

```

PR 15-SEP-2000; 2000US-0232831P.
XX (PEAR-) PHARMEXA AS.
XX
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX
XX WPI; 2002-383033/41.
XX N-PSDB; ABK51133.
XX
XX Inducing immune response against autologous immunoglobulin E in an
XX animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
XX epitope an/or B-cell epitope derived from the immunoglobulin.
XX
XX Disclosure; Page 108-110; 151pp; English.
XX
XX This invention relates to a novel method for inducing an immune response
XX against autologous immunoglobulin E (IgE) in an animal. The method
XX comprises effecting simultaneous presentation of cytotoxic T lymphocyte
XX (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
XX (TH) epitope which is foreign to the animal, by antigen
XX presenting cells (APCs) of the animal's immune system. The epitopes of
XX the invention may be used as a vaccine against allergic diseases. The
XX method of the invention is useful for inducing an immune response against
XX autologous IgE in an animal, which is useful for downregulating
XX autologous IgE in the animal. This method is useful in the prevention and
XX treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
XX asthma and atopic dermatitis. The present sequence represents the human
XX IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian
XX system, this sequence was used to create the epitopes of the invention
XX
SQ Sequence 323 AA;

Query Match          56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTWLDGQEAENLFPVYTRPKREG 81
DB 6 PPTVKILQSCDGGHFPPTIQLCLVSGYTGCTINITWLDGQVMD--VDLSTASTTQE 63

QY 82 GQTFSLQSEVNIQTGOWMSNTYTCHVKNGSIFEDSSRKCADSNPRGVSAVLSRPSF 141
DB 64 GELASTQSELTLSQKHLSDRTYTCQVYQGHTEFDSSTKCADSNPRGVSAVLSRPSF 123

QY 142 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 201
DB 124 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 183

QY 202 RWDIEGTYQCRVTHPHLPRALMRSTTKLPKRLAPEVYMLPSPSETGT--TRVTCL 259
DB 184 RWDIEGTYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF--ATPEWFGSRDKRTLACLI 242

QY 260 RGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLVNSIWEKGNLVC 319
DB 243 QNFMPEDISVQWLNHEVQLPDARHSTTPRKTKGS--GFVFSRLVETRAEWEQKDEFIC 300

QY 320 RVVHEALPGSRTLEKSLHYSAG 341
DB 301 RAVHEAASPQTQVRAVSNPG 322

RESULT 14
AAU80284
XX AAU80284 standard; protein; 323 AA.
XX
XX AAU80284;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human IgE heavy chain C2-C3-C4 domains.
XX
XX IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
XX antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
XX

```

Qy	82	QGTFS:QSEVNTTQGMGNSNTYTCHVKHNGSIFEDSSKCADSNPRGVSAYLSRSPFD	141
Db	64	GELASTQSELTLSQKHWSLDRVTTCQVYQCHTFEDSTKKCADSNPRGVSAYLSRSPFD	123
Qy	142	LFIRKSPITICLVVDLAPSKGTVNLTSASGKPNVHSTRKEEKORNGTLTITSLPVG	201
Db	124	LFIRKSPITICLVVDLAPSKGTVNLTSASGKPNVHSTRKEEKORNGTLTITSLPVG	183
Qy	202	RDWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVVMPLPSPPEETGT--TRTVTCL	259
Db	184	RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAAPEVYAF--ATPEWPSGRDKRTLACLI	242
Qy	260	RGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLVNSIWEKGNLVTC	319
Db	243	QNFMPEDISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLVNSIWEKGNLVTC	319
Qy	320	RVVHEALPGSRITLKSLSHSAG 341	
Db	301	RAVHEAASPQIVQRAVSVPNG 322	
RESULT 15			
AA883559			
ID	AA883559	standard; protein; 324 AA.	
XX	AA883559;		
XX	06-MAR-1996	(first entry)	
DI	FC(epsilon)	CH2'-CH4 protein sequence.	
DE	FC(epsilon)	; antibody; human; myeloma; probe; IgE; tryptophan promoter;	
XX	KW	constant heavy region; E.coli; glycosylation; antigenic; immunogenic;	
KW	KW	histamine; anti-allergenic; vaccine; immune response.	
XX	OS	Synthetic.	
XX	FR2715304-A1.		
XX	28-JUL-1995.		
XX	26-JAN-1994;	94FR-00000846.	
XX	26-JAN-1994;	94FR-00000846.	
PR	(INMR)	PASTEUR MERIEUX SERUMS & VACCINS.	
XX	Hurpin CM,	Panero MJM;	
XX	WPI;	1995-265243/35.	
DR	N-PSDS;	AA101865.	
XX	Antiallergic vaccine contg.	polypeptide fragment of IgE heavy chain - has	
PT	epitope(s)	not present in native IgE, also derived antibodies for	
PT	treatng or preventing	allergies, inflammatory immune disease, etc.	
XX	Claim 3;	Page 32-33; 44pp; French.	
XX	The amino acid sequence	of the Fc(epsilon) CH2'-CH4 fragment covering	
CC	amino acids 226-547.	The DNA sequence was isolated from a human myeloma	
CC	266BL cDNA library	screened with a probe corresp. to the N-terminus of	
CC	IgE. The region encoding	amino acids 218-547 was cloned into the vector	
CC	pWR11 under control	of the tryptophan promoter. The resultant protein	
CC	produced contains	some non-Fc amino acids. These were removed by	
CC	replacing their coding	sequence with a bicistronic linker. The resultant	
CC	construct encodes	the Fc(epsilon) constant heavy region from amino acids	
CC	226-547. When it is	expressed in E.coli, the protein produced is a non-	
CC	glycosylated Fc(epsilon)	fragment. Altering the pattern of glycosylation	
CC	unmasks new antigenic	sites thus rendering the Fc fragment immunogenic	
CC	and able to induce	antibodies that recognise native IgE but do not form	
CC	histamine-releasing	complexes. The Fc fragments can be used in anti-	
CC	allergenic vaccines	to modulate the intensity of immune responses	
CC	mediated by IgE		

```
XX SQ Sequence 324 AA;
Query Match 56.0%; Score 1038.5; DB 2; Length 324;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

Qy 22 PPTVKLFHSGCDPRGDHSTIQLLCLVSGFSPAKVHVTVLWDGQAEHLFPYTTTRPKREG 81
Db 7 PPTVKLIQSSCDGGHFPFTIQLLCLVSGYTFGTINITWLEDQVMD--VDLSTASTTQE 64

Qy 82 GQTFSLQSEVNITQGWMSNTVYCHVKNGSIFEDSSKCADSNPRGVSAVLSRPSPPD 141
Db 65 GELASTQSELTLQKHWLSDRTYTCQVYQGHTEFEDSTKKCADSNPRGVSAVLSRPSPPD 124

Qy 142 LFIRKSPITITCLAVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTITSLPVGT 201
Db 125 LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTITSLPVGT 184

Qy 202 RDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEETGT--TRTVCLII 259
Db 185 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVIYAF-ATPEWPGSRDKRTLACII 243

Qy 260 RGFYPSFISVOMLFNNEEDHTGHHTTRPKQKHGTDPSFFLYSRMLVNSIWEKGNLYTC 319
Db 244 QNFMPEDISVQWLHNEVQLPDARHSTQPRKTKGS--GFFVFSRLEVTAEWEQKDETC 301

Qy 320 RVVHEALPGSRTLEKSLHYSAG 341
Db 302 RAVHEAASPSTQVORAVSVNPG 323
```

Search completed: November 14, 2004, 15:06:52  
Job time : 81 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: November 14, 2004, 15:06:56 ; Search time 79 Seconds  
(without alignments)  
1531.723 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EFHHHHHTLSLPESGPVTI.....HEALPGSRTELBKSLHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1219554

Minimum DB seq length: 0

Maximum DB seq length: 342

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1856	100.0	342	9	US-09-401-636-8
2	1856	100.0	342	14	US-10-176-664-8
3	1856	100.0	342	15	US-10-673-594-8
4	1786	96.2	338	15	US-10-438-794-6
5	1786	96.2	338	15	US-10-453-915-6
6	1644.5	88.6	341	9	US-09-401-636-11
7	1644.5	88.6	341	14	US-10-176-664-11
8	1644.5	88.6	341	15	US-10-673-594-11
9	1587.5	85.5	341	9	US-09-401-636-3
10	1587.5	85.5	341	14	US-10-176-664-3
11	1587.5	85.5	341	15	US-10-673-594-3
12	1568.5	84.5	341	9	US-09-401-636-9
13	1568.5	84.5	341	14	US-10-176-664-9

14	1568.5	84.5	341	15	US-10-673-594-9	Sequence 9, Appli
15	1553.5	83.7	341	9	US-09-401-636-4	Sequence 4, Appli
16	1553.5	83.7	341	14	US-10-176-664-4	Sequence 4, Appli
17	1553.5	83.7	341	15	US-10-673-594-4	Sequence 4, Appli
18	1528.5	82.4	341	9	US-09-401-636-6	Sequence 6, Appli
19	1528.5	82.4	341	14	US-10-176-664-6	Sequence 6, Appli
20	1528.5	82.4	341	15	US-10-673-594-6	Sequence 6, Appli
21	1519	81.8	342	9	US-09-401-636-5	Sequence 5, Appli
22	1519	81.8	342	14	US-10-176-664-5	Sequence 5, Appli
23	1519	81.8	342	15	US-10-673-594-5	Sequence 5, Appli
24	1498.5	80.7	337	15	US-10-438-794-3	Sequence 3, Appli
25	1498.5	80.7	337	15	US-10-453-915-3	Sequence 3, Appli
26	1038.5	56.0	320	10	US-09-847-208-6	Sequence 6, Appli
27	1038.5	56.0	320	14	US-10-000-439-6	Sequence 6, Appli
28	1038.5	56.0	323	9	US-09-949-375A-2	Sequence 2, Appli
29	1038.5	56.0	323	9	US-09-949-375A-4	Sequence 2, Appli
30	1038.5	56.0	323	9	US-09-949-375A-6	Sequence 6, Appli
31	1038.5	56.0	323	16	US-10-363-954A-2	Sequence 2, Appli
32	1038.5	56.0	323	16	US-10-363-954A-4	Sequence 4, Appli
33	1038.5	56.0	323	16	US-10-363-954A-6	Sequence 6, Appli
34	1038.5	56.0	331	9	US-09-401-636-1	Sequence 1, Appli
35	1038.5	56.0	331	14	US-10-176-664-1	Sequence 1, Appli
36	1038.5	56.0	331	14	US-10-207-655-329	Sequence 329, App
37	1038.5	56.0	331	15	US-10-673-594-1	Sequence 1, Appli
38	1036.5	55.8	330	9	US-09-949-375A-10	Sequence 10, Appl
39	1036.5	55.8	330	16	US-10-363-954A-10	Sequence 10, Appl
40	1034.5	55.7	336	9	US-09-949-375A-8	Sequence 8, Appli
41	1034.5	55.7	336	16	US-10-363-954A-8	Sequence 8, Appli
42	791.5	42.6	220	16	US-10-704-406-3	Sequence 3, Appli
43	778.5	41.9	222	9	US-09-809-746-2	Sequence 2, Appli
44	778.5	41.9	222	10	US-09-809-715-6	Sequence 6, Appli
45	778.5	41.9	222	16	US-10-704-406-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-09-401-636-8  
; Sequence 8, Application US/09401636  
; Patent No. US20010038843A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401,636  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-8

Query Match	100.0%;	Score	1856;	DB	9;	Length	342;
Best Local Similarity	100.0%;	Pred. NO.	1.5e-139;				
Matches	342;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	EFHHHHHTLSLPESGPVTIIPVTVKLFHSSCDPRGDAHSTIQLLCVSGFSPAKVHTW	60				
Db	1	EFHHHHHTLSLPESGPVTIIPVTVKLFHSSCDPRGDAHSTIQLLCVSGFSPAKVHTW	60				
Qy	61	LVDQAEANLFPYTTREKREGGOTFSLQSEVNTTQCGWMSNTYTCHVXKNGSIFEDSSR	120				
Db	61	LVDQAEANLFPYTTREKREGGOTFSLQSEVNTTQCGWMSNTYTCHVXKNGSIFEDSSR	120				
Qy	121	KCADSNRGVSAYLSRSPEDLIRKSPITICLVLDAPSKGVNLTWSASCKPVNHS	180				

```

Db 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
QY 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY 240
Db 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY 240
QY 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
Db 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

```

## RESULT 2

```

US-10-176-664-8
; Sequence 8, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-8

```

```

Query Match 100.0%; Score 1856; DB 14; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
QY 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYTCVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYTCVKHNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
Db 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
QY 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY 240
Db 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY 240
QY 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
Db 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

```

## RESULT 3

```

US-10-673-594-8
; Sequence 8, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-8

```

```

Query Match 100.0%; Score 1856; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
QY 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYTCVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYTCVKHNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
Db 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
QY 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY 240
Db 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY 240
QY 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
Db 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

```

## RESULT 4

```

US-10-438-794-6
; Sequence 6, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated OSO
US-10-438-794-6

```

Query Match

96.2%; Score 1786; DB 15; Length 338;



Best Local Similarity 99.4%; Pred. No. 5.7e-134;  
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPSSGPTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVQGEAE 68  
DB 3 TSLPSSGPTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVQGEAE 62

QY 69 NLFPYTRPRKGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPR 128  
DB 63 NLFPYTRPRKGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPR 122

QY 129 GVSAYLSRSPDLFRKSPPTICLVVDLAPSKGTVNLTWASGKPVNHSRKEEKORN 188  
DB 123 GVSAYLSRSPDLFRKSPPTICLVVDLAPSKGTVNLTWASGKPVNHSRKEEKORN 182

QY 189 GILTVTSTLPVGRDWEIETQCRVTHPLRALMRSTTKL--PGKRLAPEVWMLPSP 246  
DB 183 GILTVTSTLPVGRDWEIETQCRVTHPLRALMRSTTKLASPGKRLAPEVWMLPSP 242

QY 247 BETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLV 306  
DB 243 BETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLV 302

QY 307 NKSIWEKGNLVCRRVHEALPGSRTLEKSLHYSAGN 342  
DB 303 NKSIWEKGNLVCRRVHEALPGSRTLEKSLHYSAGN 338

RESULT 5  
US-10-453-915-6  
; Sequence 6, Application US/10453915  
; Publication No. US20040054146A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; APPLICANT: Persson, Stefan  
; APPLICANT: Jansson, Asa  
; TITLE OF INVENTION: Allergy Vaccines  
; FILE REFERENCE: 10223-008001  
; CURRENT APPLICATION NUMBER: US/10/453,915  
; CURRENT FILING DATE: 2003-06-02  
; PRIOR APPLICATION NUMBER: 60/408,648  
; PRIOR FILING DATE: 2002-09-05  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric polypeptide  
US-10-453-915-6

Query Match 96.2%; Score 1786; DB 15; Length 338;  
Best Local Similarity 99.4%; Pred. No. 5.7e-134;  
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPSSGPTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVQGEAE 68  
DB 3 TSLPSSGPTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVQGEAE 62

QY 69 NLFPYTRPRKGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPR 128  
DB 63 NLFPYTRPRKGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPR 122

QY 129 GVSAYLSRSPDLFRKSPPTICLVVDLAPSKGTVNLTWASGKPVNHSRKEEKORN 188  
DB 123 GVSAYLSRSPDLFRKSPPTICLVVDLAPSKGTVNLTWASGKPVNHSRKEEKORN 182

QY 189 GILTVTSTLPVGRDWEIETQCRVTHPLRALMRSTTKL--PGKRLAPEVWMLPSP 246  
DB 183 GILTVTSTLPVGRDWEIETQCRVTHPLRALMRSTTKLASPGKRLAPEVWMLPSP 242

QY 247 BETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLV 306

DB 243 BETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLV 302

QY 307 NKSIWEKGNLVCRRVHEALPGSRTLEKSLHYSAGN 342

DB 303 NKSIWEKGNLVCRRVHEALPGSRTLEKSLHYSAGN 338

RESULT 6  
US-09-401-636-11  
; Sequence 11, Application US/09401636  
; Patent No. US20010038843A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401,636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-11

Query Match 88.6%; Score 1644.5; DB 9; Length 341;  
Best Local Similarity 88.0%; Pred. No. 1.1e-122;  
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60  
DB 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60

QY 61 LVDQGEAENLFPYTRPRKGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSR 120  
DB 61 LVDQGEAENLFPYTRPRKGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSR 120

QY 121 KCADSNPRGVSAYLSRSPDLFRKSPPTICLVVDLAPSKGTVNLTWASGKPVNHS 180  
DB 121 KCSEDPRGVTSVLSPPSPDLVHKAPKITCLVVDLATWEG-MNLTWYSEKPVNPGP 179

QY 181 KEEKQKNGTLVTSTLPVGRDWEIETQCRVTHPLRALMRSTTKLPGKRLAPEVY 240  
DB 180 LNKDHFNGTITVTSTLPVNTNDWIEGETYYCRVTHPLPKDIVRSIAKLPGKRLAPEVY 239

QY 241 MLPSPSEETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFL 300  
DB 240 MLPSPSEETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFFL 299

QY 301 YSRMLVNKSIWEKGNLVCRRVHEALPGSRTLEKSLHYSAGN 342  
DB 300 YSRMLVNKSIWEKGNLVCRRVHEALPGSRTLEKSLHYSAGN 341

RESULT 7  
US-10-176-664-11  
; Sequence 11, Application US/10176664  
; Publication No. US20030031663A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/10/176,664  
; CURRENT FILING DATE: 2002-06-19  
; PRIOR APPLICATION NUMBER: US/09/401,636  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02

; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-10-176-664-11

Query Match 88.6%; Score 1644.5; DB 14; Length 341;  
Best Local Similarity 88.0%; Pred. No. 1.1e-122; Indels 1; Gaps 1;  
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;  
QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
QY 61 LVDGQAEANLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCHVKHNGSIPEDSSR 120  
DB 61 LVDGQAEANLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCHVKHNGSIPEDSSR 120  
QY 121 KCADSNPRGVSAVLSRPSDFPIRKSPITITCLVVDLAPSKGTVALTWSRASKGPNVHST 180  
DB 121 KCADSNPRGVSAVLSRPSDFPIRKSPITITCLVVDLAPSKGTVALTWSRASKGPNVHST 180  
QY 121 KCSESPPRGVTSYLSPPSLDLVHKAPKITCLVVDLATMEG-MNLTWYRESKEPVNPGP 179  
DB 121 KCSESPPRGVTSYLSPPSLDLVHKAPKITCLVVDLATMEG-MNLTWYRESKEPVNPGP 179  
QY 181 RKEEKORNGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240  
DB 181 RKEEKORNGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240  
QY 180 LNKKDHFNCTITVTSTLPVNTDIEGETYQCRVTHPHLPRKDIVRSIAKLPKRLAPEVY 239  
DB 180 LNKKDHFNCTITVTSTLPVNTDIEGETYQCRVTHPHLPRKDIVRSIAKLPKRLAPEVY 239  
QY 241 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 300  
DB 240 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 299  
QY 301 YSRMLVKNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
DB 300 YSRMLVKNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

## RESULT 8

US-10-673-594-11  
; Sequence 11, Application US/10673594  
; Publication No. US20040076625A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/10/673,594  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US/05/401,636  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-10-673-594-11

Query Match 88.6%; Score 1644.5; DB 15; Length 341;  
Best Local Similarity 88.0%; Pred. No. 1.1e-122;  
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;  
QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
QY 61 LVDGQAEANLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCHVKHNGSIPEDSSR 120

DB 61 LVDGQAEANLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCHVKHNGSIPEDSSR 120  
QY 121 KCADSNPRGVSAVLSRPSDFPIRKSPITITCLVVDLAPSKGTVALTWSRASKGPNVHST 180  
DB 121 KCSESPPRGVTSYLSPPSLDLVHKAPKITCLVVDLATMEG-MNLTWYRESKEPVNPGP 179  
QY 181 RKEEKORNGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240  
DB 180 LNKKDHFNCTITVTSTLPVNTDIEGETYQCRVTHPHLPRKDIVRSIAKLPKRLAPEVY 239  
QY 241 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 300  
DB 240 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 299  
QY 301 YSRMLVKNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
DB 300 YSRMLVKNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

## RESULT 9

US-09-401-636-3  
; Sequence 3, Application US/09401636  
; Patent No. US20010038843A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401,636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-3

Query Match 85.5%; Score 1587.5; DB 9; Length 341;  
Best Local Similarity 85.4%; Pred. No. 3.8e-118; Indels 1; Gaps 1;  
Matches 292; Conservative 21; Mismatches 28;  
QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
QY 61 LVDGQAEANLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCHVKHNGSIPEDSSR 120  
DB 61 LVDGQAEANLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCHVKHNGSIPEDSSR 120  
QY 121 KCADSNPRGVSAVLSRPSDFPIRKSPITITCLVVDLAPSKGTVALTWSRASKGPNVHST 180  
DB 121 KCADSNPRGVSAVLSRPSDFPIRKSPITITCLVVDLAPSKGTVALTWSRASKGPNVHST 180  
QY 181 RKEEKORNGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240  
DB 180 LVWKEQNGTFTVTSHLPVNTDDIEGDTYTCLESPPMPVPLIRITISKAPKRLAPEVY 239  
QY 241 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 300  
DB 240 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 299  
QY 301 YSRMLVKNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
DB 300 YSRMLVKNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

## RESULT 10

US-10-176-664-3  
; Sequence 3, Application US/10176664

```
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-3

Query Match      85.5%; Score 1587.5; DB 14; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.8e-118;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
QY 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSA 120
QY 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKPVNHST 180
Db 121 KCSDTDPRGISAYILPPTQDLFVKVPTIGCLIVDLA-SAENVKVTWSRSGGPVNPSS 179
QY 181 RKEEKQKNGTLVTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
Db 181 LWKEQYNGTFTVTSHPVNTDMEIGDTYTCRLESPPDMEVPLIRTISKAPGRKLAPEVY 239
QY 241 MLPPSPETGTTRTTCCLIRGFYPSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSFFL 300
Db 240 MLPPSPETGTTRTTCCLIRGFYPSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSFFL 299
QY 301 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 342
Db 300 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 341

RESULT 11
US-10-673-594-3
; Sequence 3, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-3

Query Match      85.5%; Score 1587.5; DB 14; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.8e-118;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
QY 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSAQ 120
QY 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKPVNHST 180
Db 121 KCSDTDPRGISAYILPPTQDLFVKVPTIGCLIVDLA-SAENVKVTWSRSGGPVNPSS 179
QY 181 RKEEKQKNGTLVTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
Db 180 LVVKEQYNGTFTVTSHPVNTDMEIGDTYTCRLESPPDMEVPLIRTISKAPGRKLAPEVY 239
QY 241 MLPPSPETGTTRTTCCLIRGFYPSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSFFL 300
Db 240 MLPPSPETGTTRTTCCLIRGFYPSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSFFL 299
QY 301 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 342
Db 300 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 341

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match      84.5%; Score 1568.5; DB 9; Length 341;
Best Local Similarity 83.3%; Pred. No. 1.2e-116;
Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
QY 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKPVNHST 180
Db 121 KCSDPRGVITYLIPSPDLVYENGTPKUTCLVLDL-ESEENITVTVWRERKKSIGAS 179
QY 181 RKEEKQKNGTLVTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
Db 180 QRSTKHNATTSITSLPVDKDWIEGEGYQCRVDHHPFKPIVRSITKLPGRKLAPEVY 239
QY 241 MLPPSPETGTTRTTCCLIRGFYPSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSFFL 300
```

Db 240 MLPPSPETGTRTVTCLIRGYPSEISVQLFNNEDHTGHTTRPQKHGDTDSFEL 299

QY 301 YSRMLVNKSIWEKGNLTVCRVYHREALPGSRPLEKSLHYSAGN 342

Db 300 YSRMLVNKSIWEKGNLTVCRVYHREALPGSRPLEKSLHYSAGN 341

```

RESULT 13
US-10-176-664-9
; Sequence 9, Application US/10176664
; Publication NO. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/105,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; - OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-9

```

RESULT 14  
US-10-673-594-9  
; Sequence 9, Application US/10673594  
; Publication No. US20040076625A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OP: INVENTION, ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/10/673,594  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US/09/401,636  
; PRIOR FILING DATE: 1999-09-22

```

; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-9

```

```

RESULT 15
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; US-09-401-636-4
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-4

```

Query Match	83.7%	Score 153.5	DB 9	Length 341
Best Local Similarity	82.7%	Pred. No. 1.9e-115		
Matches 283; Conservative	21	Mismatches 37	Indels 1	Gaps 1
Qy	1	EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVGSFSAKVHVTV	60	
Db	1	EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVGSFSAKVHVTV	60	
Qy	61	LVDGQAENLFPYTTBPKSGGGTFTFSLQSEVNIQTQWMSNTYTCVHXKNGSI	120	FEDSSR

```
Db      61  LVDGQAEALFPYTTTPKKEGGQTSLQSEVNIQGWSSNTYTYCHVKHNGSIPEDSRR 120
QY      121  KCADSNPRGVAYLGRPSFDLFIKSPITITCLVVDLAPSKCTVNLTWSRASGKPVNHST 180
Db      121  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121  RCSDDEPRGVITYLIPPSPLDLYENGTPKLTCLVLDL-ESEENITVTWVREKKSIGSAS 179
QY      181  RKEEKQORNGTLTWTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240
Db      180  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      180  QRSTKHHATTSTISILPVDKDWIEGEGYQCRVDHPKPIVRSITKLPKRLAPEVY 239
QY      241  MLPPSPPEETGTRTVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 300
Db      240  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      240  MLPPSPPEETGTRTVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 299
QY      301  YSRMLVKNKSIWEKGNLVTQVWHEALPGSRTLEKSLHYSAGN 342
Db      300  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      300  YSRMLVKNKSIWEKGNLVTQVWHEALPGSRTLEKSLHYSAGN 341
```

Search completed: November 14, 2004, 15:12:43  
Job time : 80 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 15:03:41 ; Search time 24 Seconds  
(without alignments)  
1371.089 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856  
Sequence: 1 EFHHHHHTLSLPSGPVTI.....HEALFCSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 177956

Minimum DB seq length: 0  
Maximum DB seq length: 342

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: Piri:.\*  
2: Piri2:.\*  
3: Piri3:.\*  
4: Piri4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	486.5	26.2	326	1	G2HU	Ig gamma-2 chain C
2	476	25.6	327	1	G4HU	Ig gamma-4 chain C
3	473.5	25.5	328	2	I47161	Ig gamma-3 chain c
4	468	25.2	328	2	I47160	Ig gamma 2b chain
5	465	25.1	328	2	I47159	Ig gamma 2a chain
6	463.5	25.0	328	2	I47158	Ig gamma 1 chain c
7	454	24.5	330	1	GHU	Ig gamma-1 chain C
8	447	24.1	277	2	I47162	Ig gamma 4 chain c
9	443.5	23.9	322	2	FS0019	Ig gamma-2a chain
10	437.5	23.6	323	1	GHRB	Ig gamma chain C r
11	436.5	23.5	326	2	FS0017	Ig gamma-1 chain C
12	428	23.1	329	2	SC0847	Ig gamma-2c chain
13	424.5	22.9	335	1	G2GP	Ig gamma-2 chain C
14	421	22.7	335	1	G2MSAB	Ig gamma-2a chain
15	418	22.5	308	2	G30554	Ig heavy chain C r
16	415.5	22.4	324	1	G1MS	Ig gamma-1 chain C
17	413	22.3	327	2	S06611	Ig gamma-2 chain C
18	402.5	21.7	285	4	S31866	Ig gamma-1 chain C
19	401.5	21.6	289	1	G3HUWI	Ig gamma-3 heavy c
20	397	21.4	329	1	G3MSC	Ig gamma-3 chain C
21	395.5	21.3	330	1	G2MSA	Ig gamma-2a chain
22	386.5	20.8	234	2	PT0207	Ig gamma chain C r
23	384	20.7	333	2	FS0018	Ig gamma-2b chain
24	370.5	20.0	340	2	I56230	Ig alpha-2 chain -
25	369.5	19.9	340	2	B22360	Ig alpha-2 chain C
26	359.5	19.4	340	1	A2HU	Ig alpha-2 chain C
27	343.5	18.5	342	2	A45966	Ig alpha chain C r
28	318.5	17.2	342	2	I47175	Ig alpha chain C r
29	308	16.6	180	2	I46732	Ig gamma heavy cha

30 306.5 16.5 338 2 S09276  
31 298 16.1 339 2 S09264  
32 292 15.7 335 2 S09275  
33 285 15.4 152 2 S14236  
34 282 15.2 115 2 I68731  
35 280 15.1 115 2 I68727  
36 272 14.7 220 2 C22360  
37 261.5 14.1 107 2 I68726  
38 260 14.0 299 1 AHRB  
39 257 13.8 218 2 A36040  
40 253.5 13.7 107 2 I68730  
41 246.5 13.3 249 2 S69340  
42 242 13.0 228 2 S03050  
43 236.5 12.7 244 2 S12328  
44 219 11.8 111 2 S43148  
45 213.5 11.5 227 2 PH1215

## ALIGNMENTS

## RESULT 1

G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93132; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co

A:Reference number: A93906; MUID:82197621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 &lt;ELL&gt;

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:942759; PIDN:CAB58438.1;

A:Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A:Reference number: A92809; MUID:81007873; PMID:6774012

A:Contents: myeloma protein T11

A:Accession: A92809

A:Molecule type: Protein

A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 &lt;WAN&gt;

A:Note: Trp-156 is at or near the complement-binding site

R:Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; MUID:80001357; PMID:113060

A:Contents: myeloma protein Zie

A:Accession: A90752

A:Molecule type: Protein

A:Residues: 1-24,'E',26-57,'EV',60-85,132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198

A:Note: This sequence has since been revised

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A:Reference number: A93132; MUID:80114419; PMID:118920

A:Contents: Zie

A:Accession: A93132

A:Molecule type: Protein

A:Residues: 238-275 &lt;HOF&gt;

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidat

ned

R:Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
 Nature 221, 145-148, 1969  
 A;Title: Structural studies of immunoglobulin G.  
 A;Reference number: A90157; MUID:69064124; PMID:5782707  
 A;Contents: annotation; Sa, disulfide bonds  
 C;Genetics:  
 A;Gene: GDB:IGHG2  
 A;Cross-references: GDB:119338; OMIM:147110  
 A;Map position: 14q32.33-14q32.33  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;133-202/Domain: immunoglobulin homology <IM1>  
 F;239-306/Domain: immunoglobulin homology <IM2>  
 F;14/Disulfide bonds: interchain (to light chain) #status experimental  
 F;27-83,140-200,246-306/Disulfide bonds: #status experimental  
 F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.2%; Score 486.5; DB 1; Length 326;  
 Best Local Similarity 36.2%; Pred. No. 6.7e-29;  
 Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGAHSTIQLCLVSGFSPAKVHTW-----LVDGQBAENLFPYTRPKREGGQTFSLQSE 90  
 DB 16 RSTSESTAALGCLVKDYFPEPVTVMNSGALTSG---VHTFPAVL-----QSSGLYSLSSV 68

QY 91 VNTIQGWNSSNTYTCHVKH---NGSIFEDSRKCADSNP-----RGVSAYLSRSPGF 140  
 DB 69 VTPSSNF-GTQYTCNVDHKPSNTKVDKVEKCCVPCPAPVAGPSVFLFPKPK 127

QY 141 D-LFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEKQKNGTLTFTVTL 199  
 DB 128 DTLMSRTPEVTCVVDVSHEDPEVQFNWYDGVVHNAKTPREEQFNSTFRVVSULT 187

QY 200 GTRDWTEGTYQCRVTHPLPALMESTTKLPGKRLAPEVYMLPPSPPE-TGTTFTVTC 258  
 DB 188 VHODWNLNGKEYCKVSKNGLPDIETIKTKGQPREPQVYTLPPSREMTKNQVSLTCL 247

QY 259 IRGFYSEISVQWLFNNEEDHTGHTTTPQKHGTDPSFFLYSRMLVNKNSIWEKGNLVT 318  
 DB 248 VKGFYPSDIAVESNGQPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 303

QY 319 CRVVEALPGSRTLEKSLHYSAG 341  
 DB 304 CSVMHEALHNHYT-QKSLSLSPG 325

RESULT 2  
 G4HU  
 Ig gamma-4 chain C region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
 C;Accession: A90249; A02150  
 R;Ellison, J.; Buxbaum, J.; Hood, L.  
 DNA 1, 11-18, 1981  
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
 A;Reference number: A90933; MUID:83157104; PMID:6299662  
 A;Accession: A90933  
 A;Molecule type: DNA  
 A;Residues: 1-327 <ELL>  
 A;Cross-references: UNIPROT:P01861  
 A;Note: the sequence was determined from the germline gene  
 R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
 Biochem. J. 117, 33-47, 1970  
 A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of the heavy chain of human IgG.  
 A;Reference number: A90249; MUID:70207560; PMID:4192859  
 A;Accession: A90249  
 A;Molecule type: protein  
 A;Residues: 1-30;81-326 <PIN>  
 C;Genetics:

A;Gene: GDB:IGHG4  
 A;Cross-references: GDB:119340; OMIM:147130  
 A;Map position: 14q32.33-14q32.33  
 A;Introns: 99/1; 111/1; 221/1  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;20-85/Domain: immunoglobulin homology <IM1>  
 F;199-110/Region: hinge  
 F;134-203/Domain: immunoglobulin homology <IM2>  
 F;240-307/Domain: immunoglobulin homology <IM3>  
 F;14/Disulfide bonds: interchain (to light chain) #status experimental  
 F;27-83,141-201,247-305/Disulfide bonds: #status predicted  
 F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 476; DB 1; Length 327;  
 Best Local Similarity 35.8%; Pred. No. 4.1e-28;  
 Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGAHSTIQLCLVSGFSPAKVHTW-----LVDGQBAENLFPYTRPKREGGQTFSLQSE 90  
 DB 16 RSTSESTAALGCLVKDYFPEPVTVMNSGALTSG---VHTFPAVL-----QSSGLYSLSSV 68

QY 91 VNTIQGWNSSNTYTCHVKHNGSIFEDSRKCADSNP-----RGVSAYLSRSPGF 139  
 DB 69 VTPSSS-LGTYTCNVDHKPSNTKVDKVEKSGYPCPCPAPFLGPGSVFLFPKPK 127

QY 140 FD-LFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEKQKNGTLTFTVTL 198  
 DB 128 KDILMSRTPEVTCVVDVSHEDPEVQFNWYDGVVHNAKTPREEQFNSTFRVVSULT 187

QY 199 GTRDWTEGTYQCRVTHPLPALMESTTKLPGKRLAPEVYMLPPSPPE-TGTTFTVTC 257  
 DB 188 VLHQDWNLNGKEYCKVSKNGLPDIETIKTKGQPREPQVYTLPPSREMTKNQVSLTCL 247

QY 258 IRGFYSEISVQWLFNNEEDHTGHTTTPQKHGTDPSFFLYSRMLVNKNSIWEKGNLVT 317  
 DB 248 LVKGFYPSDIAVESNGQPEN--NYKTPPVLID--SDGSFFLYSKLTVDKSRWQGNVFS 303

QY 318 CRVVEALPGSRTLEKSLHYSAG 341  
 DB 304 CSVMHEALHNHYT-QKSLSLSLG 326

RESULT 3  
 147161  
 Ig gamma 3 chain constant region - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47161  
 R;Kacskovics, J.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a series of swine IgG cDNAs.  
 A;Reference number: I47158; MUID:95015845; PMID:7930579  
 A;Accession: I47161  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-328 <KAC>  
 A;Cross-references: EMBL:U03781; NID:G433127; PIDN:AAA52219.1; PID:G433128  
 C;Genetics:  
 A;Gene: IGG3  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 F;133-202/Domain: immunoglobulin homology <IM1>

Query Match 25.5%; Score 473.5; DB 2; Length 328;  
 Best Local Similarity 33.7%; Pred. No. 6.3e-28;  
 Matches 109; Conservative 59; Mismatches 128; Indels 27; Gaps 9;

QY 35 RGAHSTIQLCLVSGFSPAKVHTW-----LVDGQBAENLFPYTRPKREGGQTFSLQSE 90  
 DB 16 RDTSGPNVAGLCLASSYFPEPVTMTWNSGALTSG---VHTFPAVLQF---SGLYSLSSM 68



QY	91	UNITQGMWSSNTVTVCHVKNHNGSI	FEBOSSRK-----CADSNPRGUSAVLSRPSPF	140
Db	69	VTVPASS--LSSKSYTCNNVHPATT	KVYDKVGTNKKPPCIPCGCEVAGSFVIFPCKP	127
QY	141	D-LFRKRGPTTICLAVDLAPSGKGV	NLWTWASGKPVNHSTRKEEQORNGTITV	199
Db	128	DTLMSIQPTVTCVVVDVSKSHA	EVQFSWYVDGVEVHTAETRPKEQFNSTYRV	187
QY	200	GTRDIWEGTVOCTVTHPLRALMR	STTKLPKELAPVYVMLPPSPENGTRT--	258
Db	188	QHODWLKKEFKCKNVNDLPAP	TRISKAGQSRFPQYITLPPAEELSRSKVT	247
QY	259	IRGFVPSSISVQWLFNNEEDST	GTHHTTRPOKDHGTDPSFELYSRMLNKS	318
Db	248	VIGFYPPDIHVEWKSNGOF	PEGNYITPPQOD--VDGITFFLYSKLA	305
QY	319	CRVNHREALPGSGRTLEKSL	HYSAG 341	
Db	306	CAVMHEALHNHYT--OKSIS	KTOG 327	

RESULT 4  
I47160  
Ig gamma 2b chain constant region - pig (fragment)  
C.Species: Sus scrofa domestica (domestic pig)  
C.Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C.Accession: I47160  
R.Kaczkovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A.Reference number: I47158; NUID:95015845; PMID:7930579  
A.Accession: I47160  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-328 <YAC>  
A.Cross-references: EMBL:U033780; NID:G433125; PIDN:AAA52218.1; PID:G433126  
C.Genetics:  
A.Gene: IgG2b  
C.Superfamily: immunoglobulin C region; immunoglobulin homology  
F.I33-202/Domain: immunoglobulin homology <IMM>

Query Match	25.2%	Score	468	DB 2	Length	328			
Best Local Similarity	32.8%	Pred. No.	1.6e-27						
Matches	111	Conservative	61	Mismatches	136	Indels	30	Gaps	11
QY	22	PPYVKLPH--SSCDPRGFAHSTTQLICLVSGSPSPAKVHYTW---LVDQGEAENLFPVTT	75						
DB	2	PTAPLVYPLAPCG-RDTSGENVALGCLASSYFPEPVTVTWSGALTSG---VHTFPEVL	57						
QY	76	RPKREGGQTSLGQEVNITQGMWSSNTYCHVKNHGSIFEDSSRK-----CADS	125						
DB	58	QP-----SGLYSLSMWTVPASS-LSSKSYTCNVNHPATITKVDKVGKTRKPPCPCAC	112						
QY	126	NPRGVSAYLSRPSFD-LFIRKPTITCLVVDLAPSKGVNLTWSRAGKPVNHSRKEE	184						
DB	113	ESPQSPSVEIFPPKPKDLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTREKE	172						
QY	185	KORNGTLVTSTLPVGRDMIEGETYOCRTHPHLPALMRSTTKLPKRLAPEVYMLPP	244						
DB	173	EQFNSTYRWVSVLPIQDMLNGKEFKCKVNNKDLPAITRIISKAKGOTREPOVYTLPP	232						
QY	245	SPEETGTRR-TVTCILIGFVPSSEISVQWLFNNEEDHTGHHTTRPOKHGTDPSPFFLYSR	303						
DB	233	HAEELSRKSVGITCLVIGFPPDDIVQWQNGQPEPEGNYRTTFFQOD--VDGTVFLYSK	290						
QY	304	MLVNSKIWEKGNLVTCTRVVHEALPGSRITLKSLLHYSAG	341						
DB	291	FSVDKASMOGGGIFOCAYWHEALNHNHT-OKSISKTPG	327						

RESULT 5  
I47159

Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I471159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124  
C:Genetics:  
A:Gene: I9G2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
P:133-202/Domain: immunoglobulin homology <IMW>

Query Match	25.1%	Score 465;	DB 2;	Length 328;
Best Local Similarity	33.0%;	Pred. No. 2.7e-27;		
Matches	111;	Conservative 58;	Mismatches 137;	Indels 30; Gaps 10;
Qy	22	PPVTKLPHSSCDPRGDAHSIIQLCLVSGFSGBAKVHVTV	---	LVDQGEAENLPFYTRP 77
Db	6	PSVYPLAPCGRDTSG	---	PNVALGCLASSYFPPEVTVWNSGALSSG
Qy	78	KREGGQFSLQSEVNITQGWMSNTYTCVHKGINGSIFEDSSRK	-----	CADSNP 127
Db	60	-----SGLYSLSSMWTVPASS	---	LSKSKYTCNVNHPATTTKYDKVGTKTGPCPICPACES 114
Qy	128	RGVSAYLSRSPFD	---	LFIRKSPTITCLAVDLAPSKGTVNLTWSRASKPVNHSRKBEEK 186
Db	115	PGSVFIFPPKPKDTLMISRTPTQVCVVVDVSVQENPEVQPSWY	---	DGVEVHTAQTARPKREEQ 174
Qy	187	RNGTLTWTSLPVGTRDWIEGETVYQCBVTHPLPALMRSTTKL	---	PGKELAPEVYMLPSP 246
Db	175	FNSTYRVSVLPIQHQDMLNGKFKCKVKNKDLPAPITRI	---	SKAKGQTRBPQVYTLSPHA 234
Qy	247	EETGTR	---	TWTCILRGYPSEISVQWLFNNEDHTGHTTTRPOKDHGTPSPFELYSRML 305
Db	235	EELSRSKVSTICLVIGYPDPD	---	VEWORNQCPPEGNYRTTPFOOD
Qy	306	VNKSIMEKGNLTVCRVVHEALPGSRITLXSLHYSAG	---	341
b	293	VDKASWGGGIFOCAYVHEALHNHYT	---	OKGISKPTG 327

```

RESULT 6
I47158
IG gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47158
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03778; NID:G433121; PIDN:AA52216.1; PID:G433122
C:Genetics:
A:Gene: IG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
I:133-202/Pcmain: immunoglobulin homology <IMM>

```

Query Match 25.0%; Score 463.5; DB 2; Length 328;  
Best Local Similarity 33.9%; Pred. No. 3.5e-27;  
Matches 107; Conservative 58; Mismatches 124; Indels 27; Gaps 9;

Db 23 VALGCLASSYFPPVPTVWNSGALTSQ---VHTFSPVLQF---SGLYSLSSMTVTPASS 75  
 QY 98 WMSNTYTCVHKNGSIFEDSRK-----CADSNPRGVSAVLSRPSFD-LFIRK 146  
 Db 76 -LSKSYTCNVNHPATTTTKVDRVGHQHPQCPICPGCEVAGSFVIFPPKPKOTLMISQ 134  
 QY 147 SPRTICLVVDLAPSKGTVALTWSRAGKPVNHSRKEERQKRGTLTSTLPGVRDWE 206  
 Db 135 TPEVTCVVDVSKHAEVQFSWTVDGVEVHTAETRPKEQFNSYRVVSVLPIQHODMLK 194  
 QY 207 GETYQCRVTHPHLPRALMSTTKLPKRLAPEVYMLPPSPBETGTTR-TVTCLIRGFVPS 265  
 Db 195 GKFKCKVNVNVDLPAPITRTISAIGQSRPQVYTLPPPAEELSRSKVTLCVTGFGYPP 254  
 QY 266 EISGVQLENNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVNSKSIWEKGNLVTCRVWHEA 325  
 Db 255 DIHVWKSNGQPPENTYRTTPQDP--VDGTFFLYSKLAUDKARDHGDKECAVMEHA 312  
 QY 326 LPSRTELSLHVSAG 341  
 Db 313 LHHYTT-QKSISKTQ 327

RESULT 7  
 GHU  
 Ig gamma-1 chain C region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
 C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
 R/Billison, J.W.; Berson, B.J.; Hood, L.E.  
 Nucleic Acids Res. 10, 4071-4079, 1982  
 A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
 A/Reference number: A93433; NUID:82274238; PMID:6287432  
 A/Accession: A93433  
 A/Molecule type: DNA  
 A/Residues: 1-330 <ELL>  
 A/Cross-references: UNIPROT:P01857; EMBL:Z17370  
 A/Note: this sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) markers,  
 R/Harris, L.J.  
 submitted to the EMBL Data Library, October 1992  
 A/Reference number: S33904  
 A/Accession: S36861  
 A/Molecule type: DNA  
 A/Residues: 2-330 <HAR>  
 A/Cross-references: EMBL:Z17370  
 R/Rakahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.  
 Cell 29, 671-679, 1982  
 A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
 A/Reference number: S33887; NUID:83001943; PMID:6811139  
 A/Accession: S33987  
 A/Molecule type: DNA  
 A/Residues: 88-113;235-330 <TAK>  
 A/Cross-references: EMBL:Z17370  
 R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
 Biochemistry 9, 3161-3170, 1970  
 A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
 A/Reference number: A90563; NUID:71064024; PMID:5489771  
 A/Contents: myeloma protein Eu  
 A/Accession: B90563  
 A/Molecule type: protein  
 A/Residues: 1-96,'R',98-135 <CUN>  
 A/Note: this sequence has the Gln(3) marker, 97-Arg  
 R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
 Biochemistry 9, 3171-3181, 1970  
 A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
 A/Reference number: A90564; NUID:71064025; PMID:5530842  
 A/Contents: Eu  
 A/Accession: A90564  
 A/Molecule type: protein  
 A/Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,  
 A/Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met  
 R/Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
 A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
 igen Primärstruktur.  
 A/Reference number: A91668; NUID:77070269; PMID:826475  
 A/Contents: myeloma protein Nie  
 A/Accession: B91668  
 A/Molecule type: protein  
 A/Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
 A/Note: this sequence has the Gln(17) and Gln(1) markers  
 R/Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
 A/Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
 A/Reference number: A91723; NUID:83289131; PMID:6884994  
 A/Contents: myeloma protein KOL; disulfide bonds  
 A/Accession: A91723  
 A/Molecule type: protein  
 A/Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH  
 A/Note: this sequence has the Gln(3) and Gln(non-1) markers  
 R/Gall, W.E.; Edelman, G.M.  
 Biochemistry 9, 3188-3196, 1970  
 A/Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
 A/Reference number: A90565; NUID:71064027; PMID:4923144  
 A/Contents: annotation; disulfide bonds  
 R/Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
 A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
 enbromide cleavage products, and the disulfide bridges.  
 A/Reference number: A91667; NUID:77070267; PMID:1002129  
 A/Contents: annotation; disulfide bonds  
 C/Genetics:  
 A/Gene: GDB:IGHG1  
 A/Cross-references: GDB:120085; OMIM:147100  
 A/Map position: 14q32.33-14q32.33  
 A/Introns: 99/1; 114/1; 224/1  
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F/20-85/Domain: immunoglobulin homology <IM1>  
 F/137-206/Domain: immunoglobulin homology <IM2>  
 F/243-310/Domain: immunoglobulin homology <IM3>  
 F/27-83,144-204,250-308/Disulfide bonds: #status experimental  
 F/103/Disulfide bonds: interchain (to light chain) #status experimental  
 F/109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F/180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 24.5%; Score 454; DB 1; Length 330;  
 Best Local Similarity 34.4%; Pred. No. 1.8e-26;  
 Matches 117; Conservative 57; Mismatches 130; Indels 36; Gaps 12;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW---LVQGAEALFPYTRP 77  
 Db 6 PSVFPLAPSSKSTSG---GTAALGCLVXYDFPPTVSNNSGALTSG---VHTFPAVL-- 57  
 QY 78 KREGGQTFSLQSEVNTTQGMSSNTYCHVKNGSIFE-----DSRKC----A 123  
 Db 58 --QSSGLYSLSSVTVFSSS--LGTQTYICNVNHPKSNTKVDKVKPKSCDKTHTCPCPA 114  
 QY 124 DSNPRGVSAVLSRPSFD-LFTRKSTPITCLVVDLAPSKGTVNLTWSRASGKPVNHSK 182  
 Db 115 PELLGGPSVFLFPKPKNDTLMISRTFVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 174  
 QY 183 EEQRNGTITVTSTLPGVTRDMTEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYML 242  
 Db 175 REEQNSTYRVVSVLVTHQDMLNGEKYCKVSNKALPAPIETISKAKGQPREPQVYTL 234  
 QY 243 PPSPEE-TGTRVTVCLIRGFVPSISVQWLNFNNEEDHTGHTTTPPKDGHGTDPSFFLY 301  
 Db 235 PPSRDELTKNQVSLTCLVKGFPSPDFAVEENSGQPEN--NYKTTPEVLVD--SDGSFFLY 290  
 QY 302 SRLVNVKSIWEKGNLVTCRVTHPLPALMRSTTKLPKRLAPEVYML 341  
 Db 291 SKLTVDKSRWQGNQNVFSCSWHEALHNHVT-QKSLSLSPG 329

```

F;20-84/Domain: immunoglobulin homology <IMM>

Query Match      23.9%; Score 443.5; DB 2; Length 322;
Best Local Similarity 34.4%; Pred.No.1.1e-25;
Matches 110; Conservative 50; Mismatches 127; Indels 33; Gaps 12;

Qy 38 AHSTIQLLCVSGFSFPAKVHTV---LVGQEAENLPVTRPKREGQGFSLQSEVNI 93
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 19 SNSWVLGCLVKGYPPEPVTVWNSGALSSG---VHTFFPAVLQ-----SGLYTLTSSVTV 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 94 TQGSWMSNTYTHCVKINGSIFEDSS---RKCADSNPRGV-----SAYLSRSPSPFD-L 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 PSSTW-SSQAVTCNVAHPASSTVKDKIIVPREC---NPGCGTGSSEVSFVFPFKTKDVL 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 FIRKSPITCLVVDLAPSKGTNVLTWSRASGKPNVHSTRKEEKORNGTLTVTSTLPVQTR 202
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 TILTPKVTQVVDISQNDPEVPSFVIDDVVHTAQTHAPEKOSNLTLSRVSELPVHR 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 203 DWIETGYQCRVTHPLPRALMRSTTKLPGRLAPEVY-MLPPSPETGTTTRTTCILRG 261
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 DWLNGTKFKCKVNSGAPPAPIEKISIKSPEGTGPRGPQVYTNMAPKEENTQSOSTCMVKG 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Qy      262 FYSEISVQLFNNEDHTTHTRQQKHGTDPSFFLYSRMLVNKSIIEKGMLVTGRV 321
         ||| : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      247 FYPDIYETWKMGQPQE-::NYKNTPPTMD--TDGSFYELSKLVNKRKETWQGNTFTCSV 302
         ||| : | | : | | : | | : | | : | | : | | : | | : | | : | |

Qy      322 VHEALPGSRTLEKSLSHYSAG 341
         :||| : | | : | | : | | : | | : | | : | | : | | : | | : | |

Db      303 LFEGLNHNHT-EKSLSHSPG 321
         :||| : | | : | | : | | : | | : | | : | | : | | : | | : | |

RESULT 10
GHRB
Ig gamma chain C region - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C/Accession: A91749; A90290; F53928; A90245; A94416; A02I61
R/Bernstein: K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 19, 387-397, 1983
A/Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplo-
A/Reference number: A91749; MUID:84030930; PMID:6313520
A/Accession: A91749
A/Molecule type: mRNA
A/Residues: 1-323 <BER>
A/Cross-references: UNIPROT:P01870
```

K;Pratt, D.M.; Mole, L.E.  
Biochem. J. 151, 337-349, 1975  
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G.  
A;Reference number: A90290; PMID:76135469; PMID:1243651  
A;Accession: A90290  
A;Molecule type: Protein  
A;Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>  
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
A;Title: Heavy chain genes of rabbit IGG; isolation of a cDNA encoding gamma heavy chain.  
A;Reference number: A93288; PMID:83299917; PMID:6133512  
A;Accession: A93288  
A;Molecule type: mRNA  
A;Residues: 88-103, 'N', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
A;Cross-references: GB:W6426; NID:G165111; PID:AA34289-1; PID:G165112  
A;Note: This sequence has the dII allotypic marker, 104-Met, and the e1s allotypic mark  
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
Biochem. J. 116, 249-259, 1970  
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.  
A;Reference number: A90245; PMID:70110015; PMID:5461106  
A;Accession: A90245  
A;Molecule type: Protein  
A;Residues: 132-143, 'E', 145-161 <FRU>  
R;Hall, R.B.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell  
A;Reference number: A94416  
A;Accession: A94416

A:Molecule type: protein  
A:Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',  
A>Note: this has the e15 allelotypic marker, 185-Ala  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-92/Domain: immunoglobulin homology <IM1>  
F;130-199/Domain: immunoglobulin homology <IM2>  
F;236-303/Domain: immunoglobulin homology <IM3>  
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.6%; Score 437.5; DB 1; Length 323;  
Best Local Similarity 34.3%; Pred. No. 2.9e-25;  
Matches 113; Conservative 61; Mismatches 110; Indels 45; Gaps 14;

QY 36 GDA-HSTIQLLCVGVSPAKVHVW-----LVDGQAEANLPPYTRPKREGQTFSLQSE 90  
DB 16 GUTPSSVTGLGLVKGYPVPTVWNSGTLTGVRT---PPSV----RQSSGLYSLSSV 68  
QY 91 VNITQGWSSNTYTCHVKH-----NGSIFEDSSRXCADSNR---GVGAYLSRPPPF 140  
DB 69 VSVTS-----SSQVTCNVAPHTATKVDKTVAPSCPTCPPELLGCPSPVFPPKPK 124  
QY 141 D-LFIRKSPITICLVVDLAPSKGTNLTW-----SRASGKPVNHSRKEKQKRNGLTV 193  
DB 125 DTLMSRTPTEVTCVVDVSDQDPEVQFTWYINNEQVTRARPL-----REQQFNSTIRV 178  
QY 194 TSTLPVGTWDEGETYQCRVTHPLPALMRSTTKLPKRLAPEVY-MLPPSPREETGTT 252  
DB 179 VSTLPITHQDMURGEFKCKVKNKALPAPIETISKARGQPLEKPYVYMGPPRELSSRS 238  
QY 253 RVTCLIRGFYSEISVQWLFNNEEDHTGHTTTRPKQDHGTPSPFLYSLRMLNKSWE 312  
DB 239 VSLTCMNGFYPSDISVEKNGKAE--DNYKTTTAVLD--SDGSYFLYNKLSVPTSEWQ 294  
QY 313 KGNLTVCRVWHEALPGSRLEKSLHYSAG 341  
DB 295 RGDVFTCSVMHEALHNHT--QKSISRSPG 322

RESULT 11  
IG gamma-1 chain C region - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: PS0017; C25941  
R:Brueggemann, M.  
Gene 74, 473-482, 1988  
A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.  
A:Reference number: PS0017; MUID:89232738; PMID:3149946  
A:Accession: PS0017  
A:Molecule type: DNA  
A:Residues: 1-326 <BRU>  
A:Cross-references: UNIPROT:P20759  
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986  
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody  
A:Reference number: A25941; MUID:86287397; PMID:3016742  
A:Accession: C25941  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 220-326 <BR2>  
C:Genetics:  
A:Antons: 98/1; 113/1; 220/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F;20-84/Domain: immunoglobulin homology <IMM>

Query Match 23.5%; Score 436.5; DB 2; Length 326;  
Best Local Similarity 32.7%; Pred. No. 3.5e-25;  
Matches 105; Conservative 54; Mismatches 131; Indels 31; Gaps 10;

QY 38 AHSTIQLLCVGVSPAKVHVW-----LVDGQAEANLPPYTRPKREGQTFSLQSEVNI 93  
DB 19 SNMWTLGLVKGYPPEPTVWNSGALSSG---VHTFPAVLQ-----SGLYTLSSVTV 70  
QY 94 TQGWSSNTYTCHVKNNGSIFE-----DSSRKCADSNPRGVSAYLSRSPFP- 141  
DB 71 PSSTW-PSQVTCNVAPHTATKVDKVIKPRNGGDKPCICTGSEVSVFIPPKPRDV 129  
QY 142 LFIRKSPITICLVVDLAPSKGTNLTWNSRASGKPVNHSRKEKQKRNGLTVTSTLPVGT 201  
DB 130 LTITLPKTVCTVVDISQDDPEVHFSWFDVDEVTQAQTRPEEQFNSTFRSVSELPILH 189  
QY 202 RMIETGYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPSPBEE-TGTTTRTVTCLIR 260  
DB 190 QDLNGRTFRCKVTSAAPSPIEKTIISKPEGRQVPHVYTMSPFTKEEMTQNEVSIKCVK 249  
QY 261 GFYPSISVQWLFNNEEDHTGHTTTRPKQDHGTPSPFLYSLRMLNKSWEKGNLTVCR 320  
DB 250 GFYPPDIYVWQNGQPOE--NYKNTPTTND---TGSYFLSKLVNKKKQWQGNFTFCS 305  
QY 321 VVHEALPGSRLEKSLHYSAG 341  
DB 306 VJHEGLHNHT-EKSLSHSPG 325

RESULT 12  
S00847  
IG gamma-2c chain C region - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
C:Accession: S00847  
R:Brueggemann, M.; Delmaestro-Galfre, P.; Waldmann, H.; Calabi, F.  
Eur. J. Immunol. 18, 317-319, 1988  
A:Title: Sequence of a rat immunoglobulin gamma-2c heavy chain constant region cDNA: ext  
A:Reference number: S00847; MUID:8816903; PMID:3127222  
A:Accession: S00847  
A:Molecule type: mRNA  
A:Residues: 1-329 <BRU>  
A:Cross-references: UNIPROT:P20762; EMBL:X07189; NID:957602; PIDN:CAA30169.1; PID:g66322  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F;20-84/Domain: immunoglobulin homology <IMM>

Query Match 23.1%; Score 428; DB 2; Length 329;  
Best Local Similarity 32.4%; Pred. No. 1.5e-24;  
Matches 110; Conservative 59; Mismatches 134; Indels 36; Gaps 13;

QY 23 PTYKLFHSCDPRGDAHSTIQLLCVGVSPAKVHVW-----LVDGQAEANLPPYTRPK 78  
DB 6 PSVYPLVPGCS--GTSGSLVTLGLVKGYPPEPTVWNSGALSSG---VHTFPAVLQ-- 58  
QY 79 REGQTFSLQSEVNIQGWSSNTYTCHVKH-----NGSIFEDSSRK-----CA-D 124  
DB 59 ---SGLYTLSSSVTVFSSW--SQVTCVVAHPATKSNLIKRIEPRPKRPTDICSD 114  
QY 125 SNPRGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTNLTWNSRASGKPVNHSRKE 183  
DB 115 DNLGRPSVRFPPKPKDILMITLPKTVCVVDVSEEPQVQFSWFVDNVRVFTAQTPH 174  
QY 184 EKQNGTLTVSTLPVGTWDEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLP 243  
DB 175 EQNLNGTFRVYSTLTIHQDWMGSKGFKKVNKNKLPSPIEKTIISKPRKATPQVITIP 234  
QY 244 PSPEETGTTT-TVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQDHGTPSPFLYS 302  
DB 235 PPREQSKNKVSLTCVMTSPYASISVEWERNGLSEQ--DYKNTLPVLD--SDESFLYS 290  
QY 303 RMLVNKSWEKGNLTVCRVWHEALPGSRLEKSLHYSAG 341  
DB 291 KLSVDYDSMWRGDIYTCVVVHEALHNHT--QRNLSRSPG 328

RESULT 13

## G2GP

Ig gamma-2 chain C region - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004  
C:Accession: A94553; A90352; A90359; A90384; A90385; A02151  
R:Trischmann, T.M.  
submitted to the Atlas, April 1975  
A:Reference number: A94553  
A:Accession: A94553  
A:Molecule type: protein  
A:Residues: 1-3 <TRI>  
A:CROSS-references: UNIPROT:P01862  
R:Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
A:Reference number: A90352; MUID:71058471; PMID:5538606  
A:Accession: A90352  
A:Molecule type: protein  
A:Residues: 4-68 <BIR>  
R:Turner, K.J.; Cebra, J.J.  
Biochemistry 10, 9-17, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
A:Reference number: A90359; MUID:71058486; PMID:5538616  
A:Accession: A90359  
A:Molecule type: protein  
A:Residues: 69-133;312-329 <TUR>  
R:Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4795-4803, 1974  
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90384; MUID:75036072; PMID:4429665  
A:Accession: A90384  
A:Molecule type: protein  
A:Residues: 134-226 <TRA>  
R:Trischmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90385; MUID:75036073; PMID:4609467  
A:Accession: A90385  
A:Molecule type: protein  
A:Residues: 227-311 <TR2>  
R:Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
A:Reference number: A90354; MUID:71058474; PMID:4922544  
A:Contents: annotation; disulfide bonds  
A:Note: Cys-16 is involved in a heavy-light chain bond  
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:21-81/Domain: immunoglobulin homology <IM1>  
F:135-204/Domain: immunoglobulin homology <IM2>  
F:241-310/Domain: immunoglobulin homology <IM3>  
F:28-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:248-308/Disulfide bonds: #status experimental

Query Match 22.9%; Score 424.5; DB 1; Length 329;

Best Local Similarity 33.2%; Pred. No. 2.8e-24;

Matches 115; Conservative 52; Mismatches 136; Indels 43; Gaps 13;

QY 19 TIIPPTVKLFHSCDPRGDAHSTIQLCLVSGFSPAKVHTW----LVDGQEAENLFFYT 74

DB 4 TTAPSVFPLAASCVDTSF---SMWTGLCLVKGYPFPVTKNSGALTSF---VHTFFAV 57

QY 75 TPKREGGTFSLQSEVNTQGWSSNTYTCHVKNGSIFEDSSR----- 120

DB 58 LQ-----SGLYSLTSMVTVP-----SSQKATCNVAHPASSTKVDKTVFIRTPZBPCTC 107

QY 121 -KC-ADSNPRGSAVLSRSPFD-LFIRKSPITCLVLDLAPSKGTVNLTWASRGKPV- 176

## Db

108 PKCPPEENLGGSPVIFPPKPKDLMISLTPRTVTVVVDVSDQDEPVQTFW-VDNKPVG 166  
QY 177 NHSTKEKEKQKNGTITVTISTLPVGRDWEGETYQCRVTHPLPALMRSTTKLPKRLA 236  
DB 167 NAEETPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKYKNAKALPAPIEKTISKTKGAPRM 226  
QY 237 PEVYMLPPSPBETGTR-TVTCILRGFYPSISVQWLFNNEEDHTGHHTTTPQKDXGTD 295  
DB 227 PDVYTLPPSRDELSSKSVTCLLINFFPAIHVWASNRVPVSEKYEKNTPTPED--AD 284  
QY 296 PSFFLYSRMLVKNKSIWEKGNLVTRCVHEALPGSRTEKSLHYSAG 341  
DB 285 GSYFLYSLKTVDKSAWDQGTVTYTCVMHEALHNHVT-QKAISRSPG 329

## RESULT 14

## GZMSAB

Ig gamma-2a chain C region, secreted form (allele b) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
C:Accession: A02153; A32656  
R:Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, D.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981  
A:Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and Ig  
A:Reference number: A02153; MUID:82037861; PMID:6170065  
A:Accession: A02153  
A:Molecule type: mRNA  
A:Residues: 1-335 <SCH>  
A:CROSS-references: UNIPROT:P01864; GB:J00479  
A:Experimental source: strain C57BL/6  
R:Dognin, M.J.; Lauwereys, M.; Strosberg, A.D.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981  
A:Title: Multiple amino acid substitutions between murine gamma 2a heavy chain FC regio  
A:Reference number: A32656; MUID:8203777; PMID:6794027  
A:Accession: A32656  
A:Molecule type: protein  
A:Residues: 118-267, 'E', 269-328, 'G', 330-334 <DOG>  
C:Comment: Lys-335 is removed posttranslationally.  
C:Complex: The sequence differs from that of the allele, from BALB/c mice, at 15% of  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob  
F:98-118/Region: hinge  
F:142-211/Domain: immunoglobulin homology <IM2>  
F:248-315/Domain: immunoglobulin homology <IM3>  
F:15/Disulfide bonds: interchain (to light chain) #status predicted  
F:27-82,149-209,255-313/Disulfide bonds: #status predicted  
F:108,117/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.7%; Score 421; DB 1; Length 335;

Best Local Similarity 31.7%; Pred. No. 5.2e-24;

Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;

QY 36 GDAHSTIQLCLVSGFSPAKVHTW----LVDGQEAENLFPYTRPKREGGQTFSLQSEV 91

DB 17 GTTGSVTLGLVKGYPFPVTTWNSGSLSSGVH-----TFPALLOSGLYTLSSSV 68

QY 92 NITGQWSSNTYTCHVKNGSIFEDSSRKCADSNR----- 128

DB 69 TVTSNTW-PSQITCNVAHPAS---STKVDKIEPRVPIQPCPPHQRPVPCAAPDLL 123

QY 129 -GYSAYLSRSPFD-LFIRKSPITCLVLDLAPSKGTVNLTWASRGKPVNHSTRKEEK 186

DB 124 GGSVFIFPPKIKDVLIMISLSPMVTGVVDVSEDDPDVQISVFNWVNEVHTAQTHRED 193

QY 187 RNTGLTVTPLVGRDWEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSP 246

DB 184 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNALPSIEKTIKPRGFPVAPQVVLPPPA 243



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 15:03:40 ; Search time 97 Seconds  
(without alignments)  
2028.641 Million cell updates/sec

Title: US-09-401-636-8  
Perfect score: 1856  
Sequence: 1 EPHHHHTLSLPESGPVIT.....HEALPGSRTLKSLHYSGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1224946

Minimum DB seq length: 0

Maximum DB seq length: 342

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486.5	26.2	326	1 GC2_HUMAN	P01859 homo sapien
2	482.5	26.0	337	2 Q95M34	Q95M34 equus caball
3	476	25.6	337	1 GC4_HUMAN	P01861 homo sapien
4	454	24.5	330	1 GC1_HUMAN	P01857 homo sapien
5	443.5	23.9	322	1 GCA_RAT	P20760 rattus norv
6	437.5	23.6	323	1 GC_RABIT	P01870 oryctolagus
7	436.5	23.5	326	1 GCI_RAT	P20759 rattus norv
8	428	23.1	329	1 GC2_RAT	P20762 rattus norv
9	424.5	22.9	329	1 GC2_CAVPO	P01862 cavia porce
10	421	22.7	335	1 GCAB_MOUSE	P01864 mus musculus
11	415.5	22.4	324	1 GC1_MOUSE	P01868 mus musculus
12	401.5	21.6	290	1 GC3_HUMAN	P01860 homo sapien
13	399.5	21.5	336	1 GCB_MOUSE	P01866 mus musculus
14	397	21.4	329	1 GC3_MOUSE	P22436 mus musculus
15	395.5	21.3	330	1 GCRA_MOUSE	P01863 mus musculus
16	384	20.7	333	1 GCB_RAT	P20761 rattus norv
17	369.5	19.9	340	1 ALC2_HUMAN	P01877 homo sapien
18	334.5	18.0	303	2 Q6KAM2	Q6KAM2 mus musculus
19	334.5	18.0	303	2 BAD21435	BAD21435 mus muscu
20	260	14.0	299	1 ALC_RABIT	P01879 oryctolagus
21	228	12.3	169	2 BAD00198	BAD00198 camelus d
22	224	12.1	190	2 BAD00199	BAD00199 camelus d
23	177.5	9.6	156	2 BAD00197	BAD00197 camelus d
24	176	9.5	234	2 AAH30813	AAH30813 homo sapi
25	173.5	9.3	240	2 BAC85234	BAC85234 homo sapi
26	173	9.3	236	2 Q6PIT5	Q6PIT5 homo sapien
27	173	9.3	236	2 Q6GMX9	Q6GMX9 homo sapien
28	173	9.3	236	2 AAH29444	AAH29444 homo sapi
29	167.5	9.0	268	2 Q90524	Q90524 ginglymosto
30	166.5	9.0	236	2 Q6PIH7	Q6PIH7 homo sapien
31	166.5	9.0	236	2 AAH34141	AAH34141 homo sapi

32 166.5 9.0 237 2 Q90545 Q90545 ginglymosto  
33 165.5 8.9 267 2 Q90529 Q90529 ginglymosto  
34 165 8.9 236 2 Q723Y4 Q723Y4 homo sapien  
35 164 8.8 236 2 Q6GMX8 Q6GMX8 homo sapien  
36 163 8.8 236 2 Q6GMX0 Q6GMX0 homo sapien  
37 162.5 8.8 239 2 Q6P491 Q6P491 homo sapien  
38 162.5 8.8 239 2 AAH63599 AAH63599 homo sapi  
39 162 8.7 236 2 Q6GMW1 Q6GMW1 homo sapien  
40 160.5 8.6 259 2 Q90530 Q90530 ginglymosto  
41 160 8.6 234 2 Q72473 Q72473 homo sapien  
42 159.5 8.6 235 2 BAC85358 BAC85358 homo sapi  
43 159 8.6 234 2 Q6GMW3 Q6GMW3 homo sapien  
44 158 8.5 103 1 LAC\_CHICK LAC\_CHICK gallus gall  
45 158 8.5 236 2 BAC85236 BAC85236 homo sapi

#### ALIGNMENTS

##### RESULT 1

GC2\_HUMAN ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE 1g gamma-2 chain C region.  
GN Name=IGHG2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=8604948;  
RA Ellison J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=83001943; PubMed=6811139;  
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";  
RL Cell 29:671-679(1982).  
RN [3]  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=80001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";  
RL Can. J. Biochem. 57:759-767(1979).  
RN [6]  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920;

RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
RL immunoglobulin gamma chains.";  
RL Mol. Immunol. 16:923-925(1979).  
[7]  
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
RA Hofmann T., Parr D.M.;  
RL Submitted (MAR-1980) to the PIR data bank.  
[8]  
RN SEQUENCE OF 1-121 (DOT).  
RP MEDLINE=9535298; PubMed=7737130;  
RA Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
RT immunoglobulins.";  
RL Eur. J. Biochem. 228:886-893(1995).  
[9]  
RN DISULFIDE BONDS.  
RP MEDLINE=72033500; PubMed=4940472;  
RA Milstein C., Frangione B.;  
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
RL Biochem. J. 121:217-225(1971).  
[10]  
RN DISULFIDE BONDS.  
RP MEDLINE=69064124; PubMed=5782707;  
RA Frangione B., Milstein C., Pink J.R.L.;  
RT "Structural studies of immunoglobulin G.";  
RL Nature 221:145-148(1969).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC at the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC ENBL; J00230; AAB59393.1; -.  
DR PIR; A93906; G2HU.  
DR HSP; P01857; LOOX.  
DR Genew; HGNC:5526; IGHG2.  
DR MIM; 147110; -.  
DR GO; G0:0005624; C-membrane fraction; NAS.  
DR GO; G0:0003823; F-antigen binding; TAS.  
DR GO; G0:0006955; P-immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGH1; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Direct protein sequencing; Immunoglobulin C region;  
KW Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CHI.  
FT DOMAIN 99 110 Hinge.  
FT DOMAIN 111 219 CHI.  
FT DOMAIN 220 326 CHI.  
FT DISULFID 14 14 Interchain (with a light chain).  
FT DISULFID 27 83 Interchain (with a heavy chain).  
FT DISULFID 102 102 Interchain (with a heavy chain).  
FT DISULFID 103 103 Interchain (with a heavy chain).  
FT DISULFID 106 106 Interchain (with a heavy chain).  
FT DISULFID 109 109 Interchain (with a heavy chain).  
FT DISULFID 140 200 Interchain (with a heavy chain).  
FT DISULFID 246 304  
FT SITE 156 156  
FT VARIANT 60  
AT OR NEAR THE COMPLEMENT-BINDING SITE.  
S -> A (in myeloma proteins TIL and ZIE).  
C -> S (in Ref. 3).  
/FTID=VAR\_003889.  
FT CONFLICT 109 109  
FT SEQUENCE 326 AA; 35984 MW; 8310878C6878CF9C CRC64;  
Query Match 26.2%; Score 486.5; DB 1; Length 326;  
Best Local Similarity 36.2%; Pred. No. 2.4e-29;  
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;  
QY 35 RGDASTIQLCLVSGFSPAKVHTW-----LVDGQAEANLFPYTRPKREGGQTSLOSE 90  
DB 16 RSTSESTAALGCLVKDYFPEPTVSNVNSGALTSG---VHTFPAVL-----OSSGLYLSLV 68  
QY 91 VNITQGMWSSNTYTCTCHVXZ---NGSIFEDSSRKCADSNP-----RGVSAYLSRSPF 140  
DB 69 VTFSSNF-CTQYTCNVDHKSNVTVDKVERKCCVECPPCPAPPVAGPSFLFPKPK 127  
QY 141 D-LPIKSPITCLVVDLAPSKGTVMNLWTSRAGKPKVNHSTRKEEKORNGTLTVSTLIV 199  
DB 128 DTLMIKRTPEVTCVVDVSHEDDEVQFNMYVDVEVHNKTKPREQFNSIFRWVSLTV 187  
QY 200 GTEDWIEGETYQCRVTHPLPRALMESTTKLPKRLAPEVYMLPPSPPEE-TGTRTRVTC 258  
DB 168 VHQDNLNGKEYCKVSKNGLPADIETIKTSKQPREPQVYTLPPREEMTKNQVSLTCL 247  
QY 259 IRGFYFSEISVQWLFNNEEDHTGHHTTTRPKDGHGTDPSFFLYSRMLVKNKSIWEKNLVT 318  
DB 248 VKGFYPSDIAVEWESNGQPEN--NYKTTPEMLD--SDGSFFLYSKLTVDKSRMQQGVFS 303  
QY 319 CRVVEALPGSRTEKSLHYSG 341  
DB 304 CSVMHEALHNHYT-QKSLSLSPG 325  
RESULT 2  
Q95M34 PRELIMINARY; PRT; 337 AA.  
ID Q95M34  
AC Q95M34  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).  
GN Name=IGHC1;  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98383416; PubMed=9717671;  
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
RA Leibold W., Radbruch A.;  
RT "Organization of the equine immunoglobulin heavy chain constant region  
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";  
RL Immunobiology 199:105-118(1998).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22172648; PubMed=12185539;  
RA Wagner B., Greiser-Wilke I., Wege A.K., Radbruch A., Leibold W.;  
RT "Evolution of the six horse IGHG genes and corresponding  
RT immunoglobulin gamma heavy chains.";  
RL Immunogenetics 54:353-364(2002).  
DR EMBL; AJ300675; CAC44624.1; -.  
DR HSP; P01857; IGHZ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00407; IGH1; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
FT NON\_TER 1 1  
FT CHAIN <1 337 immunoglobulin gamma 1 heavy chain  
FT constant region.  
FT SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFDIF6 CRC64;  
Query Match 26.0%; Score 482.5; DB 2; Length 337;  
Best Local Similarity 32.8%; Pred. No. 5e-29;  
Matches 113; Conservative 67; Mismatches 120; Indels 45; Gaps 12;



```

QY 23 PTVKLFHSCDPRGDHSTIQLCLVSGSPAKVHVW-----LVGQEAENLFPYTRPK 78
Db 6 PKVFALAPCGTSD--STVALGCLVSGYFPFVKVSMNSGLTSG---VHTFPSVL--- 57
QY 79 REGGQTFQSEVNITQGGWMSNTVCHVKNGSIFE-----DSSRKCADSN--P 127
Db 58 -QSSGFYSLSMVTVPASTW-TSETVCNVVHAASNFVKDYKIEIPDNHQKCDMSKCP 115
QY 128 R-----GVSAYLRSRPFDF-LFIRKSPITICLVVDLAPSKGTNLTWSRASKPVNH 178
Db 116 KCPAPELLGSPSVIFPPPKDMLTTRTEVTCVVVDVSQBNPDVKFNWYMDGVEVRTA 175
QY 179 STRKEKQKNGTLTSTLTPVGRDWIEGETVOCRVTHPLRALMRSTTKLPGKRLAPE 238
Db 176 TTRPKEEQNSYRVVSVRIQHODWLSGKREKCKVNNQALPQPIERTITTKGSKBQ 235
QY 239 VYMLPSPBETGTR-TVTCLRGFPYSISQVWLFNNEEDTGHHTTRPKQDHTDPS 297
Db 236 VYVLAPHPDELKSKSVTCLVKDFYPPEINIEWQSQNGOPELETKYSTITQAQD--SDGS 293
QY 298 FELYSRMLYKSWKGNLVTCRVVHEALPGSRTEKSLHYSAGN 342
Db 294 YFLYSKLSVDNRNWOOGTTFTCGVWHEALHN-----HYTKRN 330

RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-4 chain C region.
GN Name=IGHG4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Euxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18 (1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL Biochem. J. 117:33-47 (1970).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR FDB; 1AQC; X-ray; A=118-323.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; C:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003557; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.

```

```

DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON TER 1 1 CH1.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83 Interchain (with a heavy chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 25.6%; Score 476; DB 1; Length 327;
Best Local Similarity 35.8%; Pred. No. 1.5e-28;
Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGDHSTIQLCLVSGSPAKVHVW-----LVGQEAENLFPYTRPKREGGQTFQSE 90
Db 16 RSTSESTAALGCLVKDYFPEFVTVSMNSGALTSG---VHTFPAVL-----QSSGLYSLSV 68
QY 91 VNITGGWMSNTVTCVHKNGSIFEDSSRKCADSNP-----RGVSAYLSRSP 139
Db 69 VTFPSSS-LGKTYTCNVVDHKPNTKVKVESKYGPCPCPAPELGGPSVFLFPKP 127
QY 140 FD-LFIRKSPITICLVVDLAPSKGTNLTWSRASKPVNHSTRKEKQKNGTLTSTLP 198
Db 128 KDTLMISRTPEVTCVVVDVSQDEPEVQFNWVDGVEVHNAKTRPREQFNSTYRVSVLT 187
QY 199 VGFEDWIEGETVOCRVTHPLRALMRSTTKLPGKRLAPEVYMLPSPBETGTRTVTC 257
Db 188 VLHGDWLNKREYCKVSKNKGKLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTKNQVSLT 247
QY 258 LIRGFYFSEISVQWLFNNEEDTGHHTTRPKQDHTDPSFFLYSRMLYKSWKGNLV 317
Db 248 LVKGFYFSDIAVEWESNGQEN--NYKTTTPVLD--SDGSFFLYSRITVDKSRWQEGNVF 303
QY 318 TCRVVEALPGSRTEKSLHYSAG 341
Db 304 SCVYHEALHNHYT-QKSLSLSG 326

RESULT 4
GC1_HUMAN
ID GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079 (1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN BU).
EX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";

```

RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RN SEQUENCE OF 136-329 (EU).  
RP MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino  
RT acid sequence of heavy-chain cyanogen bromide fragments Hs-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RN SEQUENCE (MYELOMA PROTEIN NIE).  
RP MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein NIE). Iii. The chymotryptic  
RT peptides of the H-chain, alignment of the tryptic peptides and  
RT discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RN SEQUENCE (MYELOMA PROTEIN KOL). AND DISULFIDE BONDS.  
RP MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary  
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RN DISULFIDE BONDS.  
RP MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RN DISULFIDE BONDS.  
RP MEDLINE=77070287; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein NIE). I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RP MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -|- MISCELLANEOUS: NIE has the G1M(17) allotypic marker, 97-K, and the  
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
CC G1M(3) marker and the G1M (non-1) markers.  
CC -|- MISCELLANEOUS: NIE also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -|- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -|- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J00228; AAC82527.1; ALT\_INIT.  
DR PIR: A93433; GHU.  
DR PDB: 1A07; X-ray; H=1-103.  
DR PDB: 1D55; X-ray; B/H=1-101.  
DR PDB: 1D51; X-ray; H=1-101.

DR PDB: 1D6V; X-ray; H=1-101.  
DR PDB: 1DN2; X-ray; A/B=120-326.  
DR PDB: 1E4K; X-ray; A/B=106-329.  
DR PDB: 1FC1; X-ray; A/B=106-329.  
DR PDB: 1FC2; X-ray; D=106-329.  
DR PDB: 1FCC; X-ray; A=121-326.  
DR PDB: 1H2H; X-ray; H/K=1-330.  
DR PDB: 1I7Z; X-ray; B/D=1-103.  
DR PDB: 1IIX; X-ray; A/B=107-330.  
DR PDB: 1L6X; X-ray; A=120-326.  
DR PDB: 1OQX; X-ray; A/B=119-330.  
DR PDB: 2RCS; X-ray; H=1-103.  
DR MIM: 147100;  
DR GO: 0005624; C-membrane fraction; NAS.  
DR GO: 0003823; Frantigen binding; NAS.  
DR GO: 0006955; P-immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig; 3.  
DR PROSITE: PS50835; IG\_LIKE; 3.  
DR PROSITE: PS00290; IG\_MHC; 2.  
DR 3D-structure; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 Hinge.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83 Interchain (with light chain).  
FT DISULFID 103 103 Interchain (with heavy chain).  
FT DISULFID 112 112 Interchain (with heavy chain).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180  
FT VARIANT 97 97  
FT VARIANT 239 239 N-linked (GlcNAc...)  
FT VARIANT 241 241 K -> R (in G1M(3) marker).  
FT STRAND 23 24 /FTid=VAR\_003886.  
FT STRAND 26 33 D -> E (in G1M(non-1) marker).  
FT STRAND 38 38 /FTid=VAR\_003887.  
FT STRAND 41 41 L -> M (in G1M(non-1) marker).  
FT TURN 42 45  
FT TURN 48 49  
FT TURN 50 52  
FT STRAND 57 58  
FT TURN 59 61  
FT STRAND 62 71  
FT STRAND 73 75  
FT HELIX 76 78  
FT TURN 82 87  
FT TURN 88 91  
FT STRAND 92 97  
FT TURN 102 103  
FT STRAND 122 126  
FT STRAND 130 134  
FT TURN 136 137  
FT STRAND 141 149  
FT STRAND 157 162  
FT TURN 163 164  
FT STRAND 165 167  
FT STRAND 171 172  
FT STRAND 176 177  
FT TURN 179 180  
FT STRAND 183 190  
FT STRAND 193 197  
FT HELIX 198 199  
FT TURN 202 207





```

FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 23.5%; Score 436.5; DB 1; Length 326;
Best Local Similarity 32.7%; Pred. No. 1.7e-25;
Matches 105; Conservative 54; Mismatches 131; Indels 31; Gaps 10;

QY 38 AHSTIQLCLVSGFSPAKVHVW----LVDGQEAENLFPYTRPKRGQTSLSQSEYNI 93
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 19 SNSMVLGLCLVKGYPPEVPTVWNSGALSSG---VHTFPAVLQ-----SGLYTLTSSVTV 70

QY 94 TQGNWSSNTYCHVKGNSIFE-----DSSRKADSNPRGVSAYLSRSPED- 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 PSTW-PSQVTCNVAPASSTKVDKKVPRNCGGDKPCICTGSEVSFVFPKPKDV 129

QY 142 LFIKSPITICLVVDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTITSLPYGT 201
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 LTITLPKVTVCVVDISQDDPEVHFSMFVDDVEVHTAQTRPEEQFNSTFRSVSELPILH 189

QY 202 RDWIEGTQCRVTHPLPRALMRSTTKLPGRKLAPEVMLPSPBEE-TGTRTVTCLIR 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 QDWLNRTFRCKVTSAAFPSPIEKTIKPEGRVQPHVVTMGPTTKEMTQNEVSTCMVK 249

QY 261 GFVPSBISVQWLFNNEEDHTGHITTRPKQDHTGTPSPFLYGRMLVNSIWEKGNLVTCR 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 GFVPPDIYEWQMGQPOE--NYKNTPTPTMD--TGSYFLYKLVNKKKEKQOQNTFTCS 305

QY 321 VVHEALPGSRTEKSLHYSG 341
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 VLHEGLHNHT-EKSLSHSPG 325

RESULT 8
GCC_RAT
ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Bruggemann M., Delmastro-Galfré P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant region
cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X07189; CAA30169.1; -.
DR FIR; S00847; S00847.
DR HSP; P01864; IBOG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON TER 1 97
   DOMAIN 1 CH1.

```

```

FT DOMAIN 98 113 Hinge.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 Interchain (with a light chain).
FT DISULFID 27 82
FT DISULFID 111 111 Interchain (with a heavy chain).
FT DISULFID 113 113 Interchain (with a heavy chain).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 23.1%; Score 428; DB 1; Length 329;
Best Local Similarity 32.4%; Pred. No. 7.8e-25;
Matches 110; Conservative 59; Mismatches 134; Indels 36; Gaps 13;

QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW----LVDGQEAENLFPYTRPK 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 PSVYPLVPGCS--GTSGLVTLGLCLVKGYPPEVTVKNSGALSSG---VHTFPAVLQ-- 58

QY 79 REGQTSLSQSEVNITOGQMSNTYCHVKH-----NGSIFEDSSRK-----CA-D 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 ---SGLYTLSSSVTPSSTW--SSQVTVCSSVAHPATKSNLIKRIEPRPKPRPTDICSD 114

QY 125 SNRPGVSAYLSRSPED-LFIKSPITICLVVDLAPSKGTVNLTWASRASKPVNHSRKE 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 DNLGRPSVFIKPKKDIIMITTPKVTVCVVDVSEEDPDVQFSWFDVNVVFTAQTPH 174

QY 184 EKQRNGTLTITSLPVGTRDMEGETYQCRVTHPLPRALMRSTTKLPGRKLAPEVMTLP 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 EEQLNGTFRVSTLIHQDWMSCKEPKCKVNNKOLPSPIEKTIKPRGRKARTPQVYTP 234

QY 244 PSPEETGTR-TVTCLIRGYPSEISVQWLFNNEEDHTGHITTRPKQDHTGTPSPFLYS 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 PPREQMSKNVSLTCMVTSPFASISVEWERNLEQ--DYKNTLPVLD--SDSEYFLYS 290

QY 303 RMLVNSIWEKGNLVTCTRVVHEALPGSRTEKSLHYSG 341
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 KLSVDTDSWVRGDIYTCVVHEALHNHT-QKNLSRSPG 328

RESULT 9
GCC_CAVPO
ID - GCC_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
ON NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=7058471; PubMed=5538606;
RA Birshtein B.K., Hubsain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-
G(2). 3. Amino acid sequence of the region around the half-cystine
joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=7058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-
G(2). II. Amino acid sequence of the carboxyl-terminal and hinge
region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]

```

SEQUENCE OF 134-226.  
RX MEDLINE=75036072; PubMed=4429665;  
RA Tracey D.E., Cebra J.J.;  
RT "Primary structure of the CH2 homology region from guinea pig IgG2  
antibodies.";  
RL Biochemistry 13:4796-4803(1974).  
RN [5]  
RX MEDLINE=75036073; PubMed=4609467;  
RA Trischmann T.M., Cebra J.J.;  
RT "Primary structure of the CH3 homology region from guinea pig IgG2  
antibodies.";  
RL Biochemistry 13:4804-4811(1974).  
RN [6]  
DISULFIDE BONDS.  
RX MEDLINE=71058474; PubMed=4922544;  
RA Oliveira B., Lamm M.E.;  
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";  
RL Biochemistry 10:28-31(1971).  
RN [7]  
CC -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain  
13 inbred guinea pigs.  
CC PIR; A94553; G2GP.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00407; IGC1; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Direct protein sequencing; Glycoprotein; Immunoglobulin C region;  
KW Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DISULFID 16 16 Interchain (with a light chain).  
FT DISULFID 28 79  
FT DISULFID 105 105 Interchain (with a heavy chain).  
FT DISULFID 107 107 Interchain (with a heavy chain).  
FT DISULFID 110 110 Interchain (with a heavy chain).  
FT DISULFID 142 202  
FT DISULFID 178 178 N-linked (GlcNAc...).  
FT CARBOHYD 248 308  
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;  
Query Match 22.9%; Score 424.5; DB 1; Length 329;  
Best Local Similarity 33.2%; Pred. No. 1.4e-24;  
Matches 115; Conservative 52; Mismatches 136; Indels 43; Gaps 13;  
QY 19- TIPTPTVKUHFSSCDPRGDAHSTIQLCLVSGFSPAKVHTW----LVDGQDAENLPPT 74  
Db 4 TTAPSVFPLAASCVDTSQ---SMWTGLCLVKGYPPEPTVTKVNSGALTSQ---VHTFPV 57  
QY 75 TRPKRGCGTFSIQSVNITQGMSSNTYTCVHKNGSIFEDSSR----- 120  
Db 58 LQ-----SGLYSTSVTVP-----SSQKATCNVAHPASSTKVDKTVPIRTPZBPCTC 107  
QY 121 -KC-ADSNPRGVSAYLSRSPFD-LPIKSPITTCILVDLAPSKGTVNLTVMSRSGKPV- 176  
Db 108 PKCPPPENLGGPSVFIFPKPKDLMISLTPVTCVVDVSQDEPEVOFTWF-VDNKPVG 166  
QY 177 NHSTRKEQRNGTLTVTLPGVTDWTGEGTYOCTVTHPLPRALMESTTKLPKGLA 236  
Db 167 NAETKPRVQYNTTFVSVSLPQHQDWLGRKEFKCKVYNKALPAIEKTSKTKGAPRM 226  
QY 237 PEVYMLPPPEETGTR-TVTCILIRGFPSEISVQWLFNNEEDHTCHTTRTPQKDHGTD 295  
Db 227 PDVYTLPPSRDELKSKSVTCLINFFPADIHVEWASNRVPVSEKYEKNTPEID--AD 284  
QY 296 PSFFLYSRLMVLNYSIWEKGNLTCRVVHEALPGSRTLEKSLHYSAG 341  
Db 285 GSYFLYSKLTVDKSAWDQGVVTCVSWHEALNHNVT-QKAISRSPG 329  
RESULT 10

GCAB MOUSE STANDARD; PRT; 335 AA.  
ID GCAB\_MOUSE  
AC P01864;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig gamma-2A chain C region secreted form (B allele).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=82037861; PubMed=6170085;  
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;  
RT "Multiple differences between the nucleic acid sequences of the IgG2a  
and IgG2b alleles of the mouse.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=82037777; PubMed=6794027;  
RA Dognin M.J., Lauwereys M., Strosberg A.D.;  
RT "Multiple amino acid substitutions between murine gamma 2a heavy chain  
Fc regions of Ig1a and Ig1b allotypic forms.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- ALTERNATIVE PRODUCTS.  
CC -!- Event=Alternative splicing; Named isoforms=2;  
CC Name=Secreted;  
CC IsoId=P01864-1; Sequence=Displayed;  
CC Note=Probably the major isoform;  
CC Name=Membrane-bound;  
CC IsoId=P01865-1; Sequence=External;  
CC -!- MISCELLANEOUS: The sequence differs from that of the a allele,  
from BALB/c mice, at 15% of the positions.  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; J00479; -, NOT ANNOTATED\_CDS.  
DR PIR; A02153; G2MSAB.  
DR PDB; 1BOG; X-ray; B=1-101.  
DR PDB; 1HHG; X-ray; B=1-101.  
DR PDB; 1HH9; X-ray; B=1-101.  
DR PDB; 1HI6; X-ray; B=1-101.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW 3D-structure; Alternative splicing; Direct protein sequencing;  
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.  
FT NON\_TER 1 1  
FT DOMAIN 6 98 Ig-like 1.  
FT DOMAIN 126 225 Ig-like 2.  
FT DOMAIN 234 330 Ig-like 3.  
FT STRAND 4 4  
FT STRAND 7 11  
FT STRAND 22 33  
FT STRAND 38 41  
FT STRAND 42 45  
FT TURN 46 46  
FT TURN 48 49  
FT STRAND 50 52  
FT STRAND 56 58  
FT TURN 59 60

```

FT STRAND 61 71
FT TURN 72 77
FT STRAND 81 86
FT HELIX 87 89
FT TURN 90 90
FT STRAND 91 96
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 22.7%; Score 421; DB 1; Length 335;
Best Local Similarity 31.7%; Pred. No. 2.7e-24;
Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;

QY 36 GDAHSTIQLCLVSGSPAKVHVW----LVQGEAENLFYTRPKREGGTFSLQSV 91
DB 17 GTTGGSVTLGCLVKGYFPEPVTLTWSGSLSSGVH-----TPALLQSGLYTLSSSV 68
QY 92 NITQGGWMSNTVTCVKNGSIFEDSRKCADNPR----- 128
DB 69 TVTSNTW-PSQITICNVHPAS-----STVKDKIEPRVPIQNCPHPORVPPCAAPDL 123
QY 129 -GVSAVLSRFPSPD-LFIRKSPITICLVVDLAPSKGTNLVTSRASGKPVNHSRKEEK 186
DB 124 GGSVFIFPKIKDVLMSLSPWTCVVVDSEDDPDVQISFVNNVEVHTAQQTRED 183
QY 187 RNCGLTVSTLPGTRDNIWEGTQCRVTHPLPALMRSTTKLPCKRLAPVYMLPSP 246
DB 184 YNSTLWVSLPQHQDMSGKFEKCKVNNRALPSPIETISKPRGPVRAPOVYVLP 243
QY 247 EE-TGTRTVTCILRGFSPSEISVQWLFNNEEDHTGHTTTPQXDHGTDPSFELYSRML 305
DB 244 EMTKKEPSLTCWITGLFAETAVDWTSGRTQYKNTATVLD-----SDGSYFWYSKL 299
QY 306 VNKSWEKGNLTVCRVHPALPG---SRTLEKSL 336
DB 300 VOKSTWERSLFACSVVHVLNHLTKTISRSL 333

RESULT 11
GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]

```

```

RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a murine
myeloma gamma1 chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulfide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=Displayed;
CC Note=May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=External;
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC -----
EMBL; J00453; AAB59656.1; -
EMBL; V00795; CAA24176.1; -
PIR; A02159; GIMS.
GlycoSuiteDB; P01868; -
MGD; MGI:96446; Igh-4.
GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
GO; GO:0003823; F:antigen binding; IDA.
GO; GO:00019733; P:antibacterial humoral response (sensu Vertebrata); IDA.
GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
GO; GO:0006958; P:complement activation, classical pathway; IDA.
GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
GO; GO:00050728; P:negative regulation of inflammatory response; IDA.
GO; GO:0006910; P:phagocytosis, binding; IDA.
GO; GO:0006911; P:phagocytosis, engulfment; IDA.
GO; GO:00050778; P:positive regulation of immune response; IDA.
GO; GO:00050729; P:positive regulation of inflammatory response; IDA.
GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
GO; GO:0016068; P:type I hypersensitivity; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Alternative splicing; Direct protein sequencing; Glycoprotein;
Immunoglobulin C region; Immunoglobulin domain.
NON_TER 1 1
DOMAIN 1 97 CH1.
DOMAIN 98 110 Hinge.
DOMAIN 111 217 CH2.
DOMAIN 218 324 CH3.
DISULFID 27 82 Interchain (with a light chain).
DISULFID 102 102 Interchain (with a heavy chain).
DISULFID 104 104 Interchain (with a heavy chain).
DISULFID 107 107 Interchain (with a heavy chain).
DISULFID 109 109 Interchain (with a heavy chain).
DISULFID 138 198 N-linked (GLCNAC...)/FTId=CAR_000055.
CARBOHYD 174 174
FT DISULFID 244 302
FT CONFLICT 276 276 N -> D (in Ref. 3).
FT CONFLICT 278 278 N -> D (in Ref. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338612F3D1F2C93 CRC64;

```

Query Match	22.4%;	Score 415.5;	DB 1;	Length 324;
Best Local Similarity	31.6%;	Pred. No. 7e-24;		
Matches	106;	Conservative	60;	Mismatches 138; Indels 31; Gaps 12;

  

QY	22	PPTVKLPHSSCDPRGDAHSTIQLLCLVSGFSAPKHYHTW----	LVDGOEAEMLPYTTRP	77
DD	5	PPSV--YPLAPGSAQTNSWVTIGCLVKGVPFPVPTVTWNSGLSSG---	WHTFPAVLQ-	58
QY	78	KREGGQTFSLQSEVNIITQGGWSSNTYTCHVKHGS-----	IFDSRX-CADSNPR	128
DD	59	----SDLYTLSSSVTPSSR-RESEVTCNVAHPASSTKVDKIVPRDGGCKPCICTVPE	113	
QY	129	GVSAYLSRSPFD-LFIRKSPITTCVLVDLAPSKGTYNLTWSRAGKPNVHSTRKEEKOR	187	
DD	114	VSSVFIIPPPKQVLVLTITLTKPTCVVDISKDDPEVQFSWFVDVVEVHTAQTPRESQF	173	
QY	188	NGTLTVTSTLPVGRDMIEGETQCVTHPHPLRALMRSTTKLPGRKLAPEVYMLPPSPPE	247	
DD	174	NSTRSVSEIPIHQDWLNKEFKCRVNSAPPAPIEKTIKTKGRPKAPQVITIPPEKE	233	
QY	248	ETGTR-TVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRQKDHGDDPSEFLYSRLV	306	
DD	234	QMAQKVSILTMITDFFPDITVEWQNGQP--AENYKNTQPIMN--TNGSYFYVSKLVN	289	
QY	307	NKSTWEKGNLTVCRVVEHALPGSRSTLEKSLHVSAG	341	
DD	290	QKSNWEAGNTFTCSVLHEGLNHHT-EKSLSHSPG	323	

  

RESULT 12			
GC3_HUMAN	STANDARD;	PRT;	230 AA.
ID	GC3_HUMAN		
AC	P01860;		
AD	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DD	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	IG gamma-3 chain C region (Heavy chain disease protein) (HDC).		
DE	Name=IGHG3;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID=9606;			
OX	[1]		
RX	SEQUENCE (DISEASE PROTEIN WIS).		
RX	MEDLINE=81021548; PubMed=677477;		
RA	Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;		
RT	"Primary structure of human gamma 3 immunoglobulin deletion mutant:		
RT	gamma 3 heavy-chain disease protein Wis.";		
RL	Biochemistry 19:4304-4308(1980).		
RL	[2]		
RP	REVIEWS TO 12-97 (PROTEIN WIS).		
RX	MEDLINE=77118561; PubMed=402363;		
RX	Michaelson T.B., Frangione B., Franklin E.C.;		
RA	"Primary structure of the 'hinge' region of human IgG3. Probable		
RT	quadruplication of a 15-amino acid residue basic unit.";		
RL	J. Biol. Chem. 252:883-889(1977).		
RL	[3]		
RN	REVIEWS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).		
RX	MEDLINE=77021516; PubMed=823945;		
RX	Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;		
RA	"The amino acid sequence of 'heavy chain disease' protein ZUC.		
RT	Structure of the FC fragment of immunoglobulin G3.";		
RT	Biochem. Biophys. Res. Commun. 71:907-914(1976).		
RL	[4]		
RN	SEQUENCE FROM N.A. (DISEASE PROTEIN OWM).		
RX	MEDLINE=82247635; PubMed=6808505;		
RX	Alexander A., Steinmetz M., Barritault D., Frangione B.,		
RA	Franklin E.C., Hood L., Buxbaum J.N.;		
RT	"Gamma Heavy chain disease in man: cDNA sequence supports partial gene		
RT	deletion model.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).		
RL	CC		
CC	-!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra		
CC	interchain disulfide bond at position 7 in addition to the 11		



```
SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;
Query Match 21.6%; Score 401.5; DB 1; Length 290;
Best Local Similarity 39.5%; Pred. No. 7.3e-23;
Matches 85; Conservative 49; Mismatches 74; Indels 7; Gaps 5;

QY 129 GVSAYLSRSPED-LFIRKSPITITCLVPLAPSGVNLTWGRASGKPVNHSRKEKOR 187
DB 80 GPSVFLLFPKPKDTLMISRTPEVTCVVDSHEDDEVQFKWYDGVGVNATKPREQOF 139
QY 188 NGTLTITVSTLPVGRDWISGEYVQCRVTHPHLPRALMRSTTKLPGRKLAPEVYMLPPSPPE 247
DB 140 NSTFRVSVLTVLHQLWDLGKEYCKVSNKALPAPIETKISTKQCPREPQVYTLPPSRE 199
QY 248 E-TGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFELYSRLV 306
DB 200 EMTKNOVSITCLVKGYPSDIAVWESSQPN--NYNTTPMLD--SDGSFFLYSKLTV 255
QY 307 NKSIWEKGNLTCRVVHEALPGSRITLKSLSHSAG 341
DB 256 DKSRWQGNIFSCVMHEAL-HNRFTQKSLSLSPG 289

RESULT 13
GCB MOUSE STANDARD; PRT; 336 AA.
ID GCB MOUSE AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 19 gamma-2B chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ALLELE A).
RX MEDLINE=80120716; PubMed=6766534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
RT cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
RN [2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slighcom J.L., Blattner F.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT gamma 2b heavy chain messenger RNA.";
RL Science 206:1299-1303(1979).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=80081502; PubMed=117549;
RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT "Sequence of the cloned gene for the constant region of murine gamma
RT 2b immunoglobulin heavy chain.";
RL Science 206:1303-1306(1979).
RN [4]
RP SEQUENCE FROM N.A. (ALLELE B).
RX MEDLINE=82173203; PubMed=6803173;
RA Ollo R., Rougeon F.;
RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
RT 2a and gamma 2b chain genes.";
RL Nature 296:761-763(1982).
RN [5]
RP CARBOHYDRATE-LINKAGE SITE THR-105.
RX MEDLINE=94216359; PubMed=7512967;
RA Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
RA Irimura T., Takahashi N., Kato K., Arata Y.;
RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL J. Biol. Chem. 269:12345-12350(1994).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;

```

```
CC Name=Secreted;
CC IsoId=P01866-1; Sequence=Displayed;
CC Note=May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01867-1; Sequence=External;
CC -!- PTM: O-linked glycan consists of Gal-GalNAc disaccharide which is
CC modified with 2 sialic acid residues.
CC -!- MISCELLANEOUS: The a allele sequence is shown.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR PIR; S25057; G2MS11.
DR HSSP; P01867; 1CIC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Alternative splicing; Glycoprotein; Immunoglobulin C region;
KW Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 Ig-like 1.
FT DOMAIN 127 226 Ig-like 2.
FT DOMAIN 235 331 Ig-like 3.
FT DISULFID 15 15 Interchain (with a light chain) (By
FT similarity).
FT DISULFID 27 82 By similarity.
FT DISULFID 109 109 Interchain (with a heavy chain) (By
FT similarity).
FT DISULFID 112 112 Interchain (with a heavy chain) (By
FT similarity).
FT DISULFID 115 115 Interchain (with a heavy chain) (By
FT similarity).
FT DISULFID 118 118 Interchain (with a heavy chain) (By
FT similarity).
FT DISULFID 150 210 By similarity.
FT DISULFID 256 314 By similarity.
FT CARBOHYD 105 105 O-linked (GlcNAc...).
FT VARIANT 163 163 Q -> R (in allele B).
FT VARIANT 194 194 T -> A (in allele B).
FT VARIANT 300 300 M -> D (in allele B).
FT VARIANT 301 301 N -> I (in allele B).
FT CONFLICT 25 25 L -> S (in Ref. 2 and 3).
FT CONFLICT 36 36 S -> P (in Ref. 2 and 3).
FT CONFLICT 239 239 I -> T (in Ref. 2 and 3).
SQ SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;

Query Match 21.5%; Score 399.5; DB 1; Length 336;
Best Local Similarity 31.1%; Pred. No. 1.3e-22;
Matches 107; Conservative 61; Mismatches 139; Indels 37; Gaps 13;

QY 22 PPTVKLFHSSCDPRGD-AHSTIQLLCLVSGFSAPKAVHVTWLDGQAEALPPTTRPKRE 80
DB 5 PPSVYPLAPGC--GDTTGSSTVLGCLVKGYPESVTVTW--NSGSLSSSVH---TPFALL 57
QY 81 GGQTFSLQSEVNITQGGOMSSNTVTVCHVKINGSI-----FEDSS-----R 120
DB 58 QSGLYTMSSTVTPSSTW-PSQIVTCSVAHPASTVVDKLEPSGPISTINPCFPCKECH 116
QY 121 KCADSN-PRGVAYLSRSPFD-LFTRKSPITICLVVDLAPSGTGNLTWRSAGKPVNH 178
DB 117 KCPAPNLEGGPSVFIFPPNKKDVLMSLTPKVCVVVDVSEDDPDVQISFWANNVEVHTA 176
QY 179 STRKEEQKRGNTLVSTLPVGRDWISGEYVQCRVTHPHLPRALMRSTTKLPGRKLAPE 238
DB 177 QTQHRDYNSTRVSTLFIHQDWNWSEKFKCKVNNKDLPSPIERTISKIKGLVRAPQ 236
QY 239 VYMLPPSPFETGTR-TVTCLIRGYPSEISVQWLFNNEEDHTGHHTTRFPQKHGTDPS 297
DB 237 VYILPPPAEQLSRKDVSLTCLVGVNPGDISVWTSNGHTEE--NYKDTAPVLD--SDGS 292
QY 298 FFYYSRMLVNSKWEKGNLTCRVVHEALPGSRITLKSLSHSAG 341
DB 293 YFYISKLNMKTSKWEKTDSPSCNVRHEGLK-NYYLKRKTSRSPG 335

```

```
RESULT 14
GC3_MOUSE STANDARD; PRT; 329 AA.
ID GC3_MOUSE
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; -; NOT ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01863; 1E4X.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003066; Ig_MHC.
DR Fram; PF00047; Ig; 3.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR KW Alternative splicing; Glycoprotein; Immunoglobulin C region;
KW Immunoglobulin domain; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 Hinge.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 21.4%; Score 397; DB 1; Length 329;
Best Local Similarity 31.8%; Pred.No. 1.9e-22;
Matches 110; Conservative 53; Mismatches 142; Indels 40; Gaps 14;

QY 19 TIIPPTVKLFHSCDPRGDAHSTIQLLCVSGFSPAKVHVTV---LVDGQEAENLFYPT 74
DB 2 TIAPSVVPLVPGCDTSFG---SSVTLGCLVKGYPFEPVTVKXNYGALSSGVR-----T 51
QY 75 TRPKREGGQTFSLQSVNITQGWSSNTYTHVXNGSIFEDSR----- 120
DB 52 VSSVLQSG-FYLSLSLVTPSSTW-PSQVTCVNAVHAPASKTLIKRIEIPRIKPTPPGS 109
QY 121 KCADSN-PRGVSAYLSPSPFD-LFIRKSPITCLVLDLAPSKGVNLTWSRASGKPVNH 178
DB 110 SCPFGNLLGSPSVFIPPKPKALMSLTPKTCVVVDVSDSDPDVHVSWF-VDNKEVHT 168
QY 179 S-TRKEKORNGTLTWTSLPVGTRDWIEGETYQCRVTHPHPLRALMRSTYKLPKRLAP 237
DB 169 AWTQPEAQVNSTFRVVSALPQIQDWMRGKFKCKVNNKALPAPIERTISKPKGRAQTP 228
QY 238 EYVMLPSPSEETGTTT-TVTCILRGYPSEISVOMLFNNEEDHTGHTTTPQKHGTDTP 296
DB 229 QVTTIPFPPEQMSKKVSLTCLVTNFFSAISVERNGELSEQ--DYKNTPILD--SDG 284
QY 297 SPFLYSRMLVNKSIWEKGNLTVCRVVHVALPGSRITLKSLSHYSAG 341

RESULT 15
GCAA_MOUSE STANDARD; PRT; 330 AA.
ID GCAA_MOUSE
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multi-genic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00798; CAA24178.1; --
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; X-ray; H=1-99.
DR PDB; 1E4X; X-ray; H/I=1-103.
DR PDB; 1MNU; X-ray; H=1-103.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003066; Ig_MHC.
DR Fram; PF00047; Ig; 2.
```



**This Page Blank (uspto)**



```

Db      162  TREKNVT-STHSELNITQGEWSQKTYTCQVYQGTFFKDEARKCSSEDPRGVTSYLSPP 220
QY      138  SPFDLFIKSPITICLVVDLASKGTVNLTWSRSGKPNHSTRKEEKQKORGLTIVTSTL 197
Db      221  SPLDLVHKAPKITCLVWDLATMEG-MNLTWYRESKEFPVNPGLNKKDHFNGTITVTSTL 279
QY      198  PVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPPEETGTR--TV 255
Db      280  PVTNDWIEGETYQCRVTHPHLPKDIVRSIAKAPGRAPPDVYLFPLPEEGQIKDRVTL 339
QY      256  TCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
Db      340  TCLIQNFFPADISVQWLRNDSPIQDQYTTTGPHKVGSRPAFFIFSRLEVSRLVDEQKN 399
QY      316  LVTQVWVHEALPGSRITLKSLSHSAG 341
Db      400  KFTCQVWHEALSGSRILQKWSKTPG 425

```

## RESULT 2

```

PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

```

```

Query Match      53.3%; Score 989; DB 5; Length 426;
Best Local Similarity 56.7%; Pred. No. 1.3e-87;
Matches 185; Conservative 53; Mismatches 84; Indels 4; Gaps 3;

QY      18  VTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTLWVDGQAEANLFPYTRP 77
Db      102  LNFIPPTVKLFHSSCNFVGDTHTIQLCLISGVPGDMEVTLWVDGQKATNIFPYTAPG 161
QY      78  KREGGOTFSLQSEVNITQGMSSNTYTCVXKNGSIPEDSRKCADSNPRGVSAYLSRP 137
Db      162  TREKNVT-STHSELNITQGEWSQKTYTCQVYQGTFFKDEARKCSSEDPRGVTSYLSPP 220
QY      138  SPFDLFIKSPITICLVVDLASKGTVNLTWSRSGKPNHSTRKEEKQKORGLTIVTSTL 197

```

```

Db      221  SPLDLVHKAPKITCLVWDLATMEG-MNLTWYRESKEFPVNPGLNKKDHFNGTITVTSTL 279
QY      198  PVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPPEETGTR--TV 255
Db      280  PVTNDWIEGETYQCRVTHPHLPKDIVRSIAKAPGRAPPDVYLFPLPEEGQIKDRVTL 339
QY      256  TCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
Db      340  TCLIQNFFPADISVQWLRNDSPIQDQYTTTGPHKVGSRPAFFIFSRLEVSRLVDEQKN 399
QY      316  LVTQVWVHEALPGSRITLKSLSHSAG 341
Db      400  KFTCQVWHEALSGSRILQKWSKTPG 425

```

## RESULT 3

```

US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

```

```

Query Match      52.4%; Score 972; DB 4; Length 431;
Best Local Similarity 56.7%; Pred. No. 5.9e-86;
Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

QY      18  VTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTLWVDGQAEANLFPYTRP 77
Db      107  MNFIPPTVKLFHSSCNPLGDTGTIQLCLISGVPGDMEVTLWVDGQKATNIFPYTAPG 166
QY      78  KREGGOTFSLQSEVNITQGMSSNTYTCVXKNGSIPEDSRKCADSNPRGVSAYLSRP 137
Db      167  KQEGKVT-STHSELNITQGEWSQKTYTCQVYQGTFFEDHARKCTESDPRGVSYLSPP 225
QY      138  SPFDLFIKSPITICLVVDLASKGTVNLTWSRSGKPNHSTRKEEKQKORGLTIVTSTL 197
Db      226  SPLDLVHKSPKITCLVWDLANTDGM-LTWSRENGESVHPDPMVKKTQYNGTITVTSTL 284
QY      198  PVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPPEETGTR--TV 255
Db      285  PVDATDWIEGETYQCRVTHPHLPKDIVRSIAKAPGRFPPEVYVFLPPPEGEKTKDKVTL 344
QY      256  TCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
Db      345  TCLIQNFFPADISVQWLRNDSPIQDQYTTTGPHKATGSPAFFIFSRLEVSRLVDEQKN 404
QY      316  LVTQVWVHEALPGSRITLKSLSHSAG 341
Db      405  VFTCQVWHEALPGFRTLKKSVMKNGP 430

```

## RESULT 4

```

US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric

```

	Query Match	52.4%	Score 772	DB 4	Length 496
	Best Local Similarity	56.7%	Pred. No. 7.3e-86		
	Matches 185	Conservative	52	Mismatches 85	Indels 4
	Gaps				
QY	18	VTIIPPVKLFHSCDPRGDAHSIIQLLCVSGFSAPKAVHTVLVDQEAENLFPYITRP	77		
Db	172	MNEIIPPVKLFHSCNPLGTGTSTIIQLLCISGYVPGDMETVTLVDQKATNIPYAPG	231		
QY	78	KREGQGFSLQSEVNIITQGGWMSNTYTCVHKHNGSIFEDSSRKCAOSNPRGVSAIYLSRP	137		

Query Match	36.3%	Score	673	DB 3	Length	561			
Best Local Similarity	41.6%	Pred. No.	1e-56						
Matches	147	Conservative	53	Mismatches	133	Indels	20	Gaps	7
Qy	2	FHHHHHTLSLPSG	PVTIIPPTVKLFHS-----SCDRGDAHSTLIQLCLVSGF	51					
Db	211	FTCHVTHPPSN	RSTILVRPVT-----HSLSPWYSIHRCDPNA-FHSTLIQLCFYIGH	265					
Qy	52	SPAKVHTVWLVDQ	EAEENLPYTRPKREGQOTFSLOSEVNITOGWMSNNTYCHVKHN	111					
Db	266	ILNDVSUSWLMDD	REITDTLAQTVLKEE-GKLASTCKLNIITQOWMSESTFCRVTSQ	324					
Qy	112	GSIFESSRKCADS	NPRGVSAYLSRPSFDFLTRKSPITICLVVDLAPSKGTVNLWTRA	171					
Db	325	GVDYLAHTRCRP	DPEPRGAIYTIIPSPDLIQNGAPKLTCLVVDLSEK-NVNVNTNQE	383					
Qy	172	SGFPVNHSTRKEE	QRNGTLTVTSTLPVGRFDMTEGETYQCRVTHPHLPALMRSTTKLP	231					
Db	384	KKTSVSASQWYKH	NNNATTSITSLPVAQKMWIEGYQCVVDROPFPKPIVRSIT-LP	442					
Qy	232	--GKRLAPEVYML	PPSPPEETGTTVTRVCLIRGFYPSSEISQVWLFPNNBEDHTGHHTTRPQ	289					
Db	443	QVQSRSAPVYVVP	PPPEESSEDKTTLCTLCNFFPEDISQVWLGDGKLINSQHSITITPL	502					
Qy	290	KDHGTDPSPFLY	SRMLVKNYSIWEGKNILVTRCVVHEALPGSRTLEKSLHYSAGN	342					
Db	503	KNSGNSOGFTIF	SRLEVAKTLWTORKOFTCOVIEHALQKPKLSEKTLSTSLGN	555					

RESULT 7  
US-08-232-539D-56  
; Sequence 56, Application US/08232539D  
; Patent No. 5965709  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Ige Antagonists  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,539D  
; FILING DATE: 21-Apr-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/178583  
; FILING DATE: 07-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-232-539D-56

Query Match 31.2%; Score 579; DB 2; Length 113;  
Best Local Similarity 98.2%; Pred. No. 1.3e-48;  
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 122 CADSPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTWASGKPVNHSTR 181  
Db 1 CADSPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTWASGKPVNHSTR 60  
QY 182 KEKORNGTLVTSTLPVGTDRDIEGETYQCRVTHPHPLRALMRSTTKLPG 232  
Db 61 KEKORNGTLVTSTLPVGTDRDIEGETYQCRVTHPHPLRALMRSTTKTSG 111

RESULT 8  
US-08-466-163B-1  
; Sequence 1, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1D1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 1  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-466-163B-1

Query Match 29.6%; Score 548.5; DB 3; Length 109;  
Best Local Similarity 97.2%; Pred. No. 1.1e-45;  
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 124 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTWASGKPVNHSTRKE 183  
Db 1 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTWASGKPVNHSTRKE 60  
QY 184 EKORNGTLVTSTLPVGTDRDIEGETYQCRVTHPHPLRALMRSTTKLPG 232  
Db 61 EKORNGTLVTSTLPVGTDRDIEGETYQCRVTHPHPLRALMRSTTKTSG 108

RESULT 9  
US-09-802-096-1  
; Sequence 1, Application US/09802096  
; Patent No. 6685939  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C3US  
; CURRENT APPLICATION NUMBER: US/09/802,096  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 1  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-802-096-1

Query Match 29.6%; Score 548.5; DB 4; Length 109;  
Best Local Similarity 97.2%; Pred. No. 1.1e-45;  
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 124 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTWASGKPVNHSTRKE 183  
Db 1 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTWASGKPVNHSTRKE 60  
QY 184 EKORNGTLVTSTLPVGTDRDIEGETYQCRVTHPHPLRALMRSTTKLPG 232  
Db 61 EKORNGTLVTSTLPVGTDRDIEGETYQCRVTHPHPLRALMRSTTKTSG 108

RESULT 10  
US-09-802-077-1  
; Sequence 1, Application US/09802077  
; Patent No. 669472  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)



```
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-1

Query Match      29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 124 DSNPRGVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKE 183
Db 1 DSNPRGVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKE 60

QY 184 EKORNGTLVTSITPLVGTDRDIEGETYQCRVTHPHLPALMESTTKLPG 232
Db 61 EKORNGTLVTSITPLVGTDRDIEGETYQCRVTHPHLPALMESTTKTSG 108

RESULT 11
US-08-232-539D-54
; Sequence 54, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 106 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-54

Query Match      29.0%; Score 538; DB 2; Length 106;
Best Local Similarity 98.1%; Pred. No. 1.1e-44;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 GVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEQRN 188
Db 1 GVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEQRN 60

QY 189 GTLTVTSTPLVGTDRDIEGETYQCRVTHPHLPALMESTTKLPG 232
Db 61 GTLTVTSTPLVGTDRDIEGETYQCRVTHPHLPALMESTTKTSG 104

RESULT 12
US-09-828-995B-38
; Sequence 38, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE Igg AND CANINE IL-13
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,859
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-38

Query Match      28.0%; Score 520.5; DB 4; Length 352;
Best Local Similarity 36.4%; Pred. No. 3.4e-42;
Matches 129; Conservative 58; Mismatches 138; Indels 29; Gaps 12;

QY 5 HHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTWLVDG 64
Db 10 HWNGTSLFVSSASTTAPSVFPLAPSCGSTG---STVALACLVSgyfpepvtvsmnsds 66

QY 65 -QEAEENLFPYTRPKREGGOTFSLQSEVNITQGWMSNTYTCHVKHGS-----IFE 116
Db 67 LTSGVHTFPVSL-----QSSGLYLSSTVTPSSRW-PSEFTCNVHPASNTKVDKEVPK 121

QY 117 DSSRKCADSNP-----RGVSAYLSRSPFDLF IRKSPITICLVVDLAPSKGTNLTWSR 170
Db 122 ESTCKCISPCVPVPSLGGSPVFPKPKDILRTRTPEITCVVLDLGDREDPEVQISWF - 180

QY 171 ASGKPVNHS-TRKEEKQKNGTLVTSTPLVGTDRDIEGETYQCRVTHPHLPALMESTTK 229
Db 181 VDGKEVHTAKTPREQQFNSTYRVVSLPIEHQDWLTGKFKPKCRVNHIGLPSPIERTISK 240

QY 230 LPGKRLAPEVYMLPPSPPEE--TGTRTIVTCLIRGFYPSSEISVQWLFNNEEDHTGHHTTR 287
Db 241 ARGQAHPVSVVLPSPKELSSSDTVTLTCLDKDFPPEIDVEWQSQNGQPEPEKHYHTA 300

QY 288 PQKDHGTDPSPFFLYSRMLVNSIWEKGNLTCTRVVHEALPGSRITLESLSHSAG 341
Db 301 PQLDE--DGSYFLYSKLSVDKSRWQQDPPTCAVMHEALQNHYT-DLSLSHSPG 351

RESULT 13
US-09-828-995B-11
```

; Sequence 11, Application US/09828995B  
; Patent No. 6703360  
; GENERAL INFORMATION:  
; APPLICANT: Heskia Corporation  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Tang, Liang A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R  
; FILE REFERENCE: AL-7  
; CURRENT APPLICATION NUMBER: US/09/828,995B  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 60/195,874  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/195,659  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 11  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-828-995B-11

Query Match 28.0%; Score 519.5; DB 4; Length 470;  
Best Local Similarity 36.4%; Pred. No. 6.5e-42;  
Matches 130; Conservative 58; Mismatches 134; Indels 35; Gaps 13;

QY 5 HHHHTLSLPSGPTVITPTVKLFHSSCDPRGDASHSTIQLCLVSGFSPAKVHTW---- 60  
DB 128 HWNGTSLFVSSASTAPVFLAPSCGTSG---STVALACLVSGYFPEPTVSWNSGS 184

QY 61 LVDGQAEALFPYTRPKEGGTFSLQSEVNITQCOMSSNTYTCHVKHGS----- 113  
DB 185 LTSG---VHTFPSVL-----QSSGLVSLSTVTPSSRW-PSETFTCNVHPASNTKVKP 236

QY 114 IFEDSRKADSNP-----RGVSAYLSRSPDPLF-IRKSPITICLVDLAPSKGTVNLT 167  
DB 237 VPKESTCKISPCVPESLGGPSVFIFPPKPKDILRITPTETVCVLDLGEDPEVQIS 296

QY 168 WSRASGKPVNHS-TRKEKORNGTLTSTLPVGTGRDWTGEGTYOCRTVHPHLPALMRS 226  
DB 297 WF-VDSKEVHTAKTQPREQFNSTYRVVSVLPIEHQDMLTGKFKCRVNHICLPSPERT 355

QY 227 TTKLPGRKLAPEVYMLPPSPER--TGTTTTCVLRGFPSPISVQWLFNNEEDHTGHT 284  
DB 356 ISKARGQAHQPSVYVLPSPKELSSSDTITLCLIKDFPPDIDVEWQSGQPEPESEKYH 415

QY 285 TTRPOKHGTDPDSFFLYSRMLYNKSTWEGNLVTCRVVHEALPGSRTLEKSLHVSAG 341  
DB 416 TTAPOQDE--DGSYFLYSLVDSKRWQGDFTTCVAMHETLQNHYT-DLSLSHSPG 469

RESULT 14  
US-09-828-995B-5  
; Sequence 5, Application US/09828995B  
; Patent No. 6703360  
; GENERAL INFORMATION:  
; APPLICANT: Heskia Corporation  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Tang, Liang A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R  
; FILE REFERENCE: AL-7  
; CURRENT APPLICATION NUMBER: US/09/828,995B  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 60/195,874  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/195,659  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 5  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Canis familiaris

US-09-828-995B-5  
Query Match 27.6%; Score 513; DB 4; Length 468;  
Best Local Similarity 36.4%; Pred. No. 2.8e-41;  
Matches 124; Conservative 58; Mismatches 121; Indels 38; Gaps 14;

QY 23 PTVKLFHSSCDPRGDASHSTIQLCLVSGFSPAKVHTW----LVDGQAEALFPYTRPK 78  
DB 143 PSVFPLAPSCG--STGSTVALACLVSGYFPEPTVSWNSGSLSG---VHTFPSVL--- 194

QY 79 REGQTFSLQSEVNITQCOMSSNTYTCHVKHGS-----IFEDSRKCADSNP----- 127  
DB 195 -QSSGLHSLSSMTVPSSRW-PSETFTCNVHPASNTKVKDPVFNEC--RCTDTPPCVP 250

QY 128 ---RGVSAYLSRSPDPLF-IRKSPITICLVDLAPSKGTVNLTWSRASGKPVNHS-TRK 182  
DB 251 EPLGGPSVLIFPPKPKDILRITPTETVCVLDLGEDPEVQISWF-VDSKEVHTAKTOS 309

QY 183 BEKORNGTLTSTLPVGTGRDWTGEGTYOCRTVHPHLPALMESTTKLPGRKLAPEVYML 242  
DB 310 REQQNGTYRVVSVLPIEHQDMLTGKFKCRVNHICLPSPERTISKARGRAHKPSVYVL 369

QY 243 PPSPETGTTRTV--TCLIRGFPSPISVQWLFNNEEDHTGHTTTTRPOKHGTDPDSFFL 300  
DB 370 PPSPKELSSSDTITLCLIKDFPPDIDVEWQSGQPEPEKHMTPPQIDE--DGSYFL 427

QY 301 YSRMLYNKSTWEGNLVTCRVVHEALPGSRTLEKSLHVSAG 341  
DB 428 YKLSVDKSRWQGDFTTCVAMHETLQNHYT-DLSLSHSPG 467

RESULT 15  
US-08-646-981-16  
; Sequence 16, Application US/08646981  
; Patent No. 5852183  
; GENERAL INFORMATION:  
; APPLICANT: MAEDA, HIROAKI  
; APPLICANT: EDA, YASUYUKI  
; APPLICANT: KINACHI, KAZUHIKO  
; APPLICANT: ONO, YOICHI  
; APPLICANT: TOKIYOSHI, SACHIO  
; TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE  
; TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,981  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEINER, MARC S  
; REGISTRATION NUMBER: 32,181  
; REFERENCE/DOCKET NUMBER: 1485-106  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 334 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-646-981-16

```
Query Match      27.6%; Score 512; DB 2; Length 334;
Best Local Similarity 35.9%; Pred. NO. 2.1e-41;
Matches 123; Conservative 60; Mismatches 122; Indels 38; Gaps 12;

QY 23 PTVKLPSSCDPRGDAHSIIQLLLVSGFSPAKVHVW----LVDQGEAENLFPVYTRPK 78
Db 5 PSVFPPLDPSCG--STSGSIVALACLVSgyfpepVTVSWNSGSLTSG-----VHTFPSD 55

QY 79 REGGQFSLQSEVNITQCGWMSNTYTCHVKH-----NGSIFE--DSSRK 121
Db 56 LQSSGLYSLSSMVTVPSSRW-SSETFTCNVAHPASKTKVDKVPKRENGRVRPRPDCPKC 114

QY 122 CADSNPRGVSAYLSRSPFD-LPIKSPITICLVVDLAPSKGTVNLTVASRASKPVNHS- 179
Db 115 PAPMLGGSPVFIFPKPKDTHLIARTPEVTCUVVDLGPEDPEVQISWF-VDGKQKQIAK 173

QY 180 TRKEEQKQNGTLVTITLPGVTRDMIEGETYQCRVTHPHLPALMRSTTKLFGKELAPEV 239
Db 174 TQPREEQFNGTVRVSVSLPIGHQDWLKGKQFTCKVNNKALPSPIERTISKARGQAHQPSV 233

QY 240 YMLPPSPPEB-TGTRTVTCLIRGFYFSEISVQWLFNNEEDHTGHHTTTPQKHGTDPSF 298
Db 234 YVLPFRRELSKNTVSLTCLIKDFPPDIDVWQSNQOQEPESKYRTTTPPQLDE--DGSY 291

QY 299 FLYSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 341
Db 292 FLYSKLSVDKSRWQRGDTFICAWHEALHNHYT-QKSLSHSPG 333
```

Search completed: November 14, 2004, 15:03:00  
Job time : 40 secs

This Page Blank (uspto)

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 15:01:45 ; Search time 144 Seconds  
(without alignments)  
840.320 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EFHHHHHTLSLPESGVVTI.....HEALPGSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353919137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap:*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap:*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap:*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1856	100.0	342	9	US-09-401-636-8
2	1856	100.0	342	14	US-10-176-664-8
3	1856	100.0	342	15	US-10-673-594-8
4	1786	96.2	338	15	US-10-438-794-6
5	1786	96.2	338	15	US-10-453-915-6
6	1786	96.2	347	15	US-10-438-794-14
7	1786	96.2	347	15	US-10-453-915-14
8	1772	95.5	557	15	US-10-438-794-12
9	1772	95.5	557	15	US-10-438-794-16
10	1772	95.5	557	15	US-10-453-915-12
11	1772	95.5	557	15	US-10-453-915-16
12	1772	95.5	566	15	US-10-438-794-10
13	1772	95.5	566	15	US-10-438-794-18

14	1772	95.5	566	15	US-10-453-915-10	Sequence 10, Appl
15	1772	95.5	566	15	US-10-453-915-18	Sequence 18, Appl
16	1759	94.8	353	15	US-10-453-915-21	Sequence 21, Appl
17	1644.5	88.6	341	9	US-09-401-636-11	Sequence 11, Appl
18	1644.5	88.6	341	14	US-10-176-664-11	Sequence 11, Appl
19	1644.5	88.6	341	15	US-10-673-594-11	Sequence 11, Appl
20	1587.5	85.5	341	9	US-09-401-636-3	Sequence 3, Appl
21	1587.5	85.5	341	14	US-10-176-664-3	Sequence 3, Appl
22	1587.5	85.5	341	15	US-10-673-594-3	Sequence 3, Appl
23	1587.5	85.5	345	9	US-09-401-636-10	Sequence 10, Appl
24	1587.5	85.5	345	14	US-10-176-664-10	Sequence 10, Appl
25	1587.5	85.5	345	15	US-10-673-594-10	Sequence 10, Appl
26	1568.5	84.5	341	9	US-09-401-636-9	Sequence 9, Appl
27	1568.5	84.5	341	14	US-10-176-664-9	Sequence 9, Appl
28	1568.5	84.5	341	15	US-10-673-594-9	Sequence 9, Appl
29	1553.5	83.7	341	9	US-09-401-636-4	Sequence 4, Appl
30	1553.5	83.7	341	14	US-10-176-664-4	Sequence 4, Appl
31	1553.5	83.7	341	15	US-10-673-594-4	Sequence 4, Appl
32	1528.5	82.4	341	9	US-09-401-636-6	Sequence 6, Appl
33	1528.5	82.4	341	14	US-10-176-664-6	Sequence 6, Appl
34	1528.5	82.4	341	15	US-10-673-594-6	Sequence 6, Appl
35	1523.5	82.1	446	14	US-10-214-524-32	Sequence 32, Appl
36	1519	81.8	342	9	US-09-401-636-5	Sequence 5, Appl
37	1519	81.8	342	14	US-10-176-664-5	Sequence 5, Appl
38	1519	81.8	342	15	US-10-673-594-5	Sequence 5, Appl
39	1498.5	80.7	337	15	US-10-438-794-3	Sequence 3, Appl
40	1498.5	80.7	337	15	US-10-453-915-3	Sequence 3, Appl
41	1486.5	80.1	555	15	US-10-438-794-8	Sequence 8, Appl
42	1486.5	80.1	555	15	US-10-453-915-8	Sequence 8, Appl
43	1285.5	69.3	427	14	US-10-214-524-36	Sequence 36, Appl
44	1050.5	56.6	343	9	US-09-401-636-7	Sequence 7, Appl
45	1050.5	56.6	343	14	US-10-176-664-7	Sequence 7, Appl

#### ALIGNMENTS

##### RESULT 1

```
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8
```

Query Match	100.0%	Score 1856	DB 9	Length 342
Best Local Similarity	100.0%	Pred. No. 1.5e-139		
Matches 342	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	EFHHHHHTLSLPESGVVTI	PPVTIKLPHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW	60
Db	1	EFHHHHHTLSLPESGVVTI	PPVTIKLPHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW	60
QY	61	LVDQEAENLFPYTRPKREGGQT	FSIQSEVNITQGMSSNTYCHVKNGSIFEDSSR	120
Db	61	LVDQEAENLFPYTRPKREGGQT	FSIQSEVNITQGMSSNTYCHVKNGSIFEDSSR	120
QY	121	KCADNSRPGVSAYLSRSPDLF	IRKSPITICLVVDLAPSKGTNLTMSRSGKPVNHS	180

Db 121 KCADSNPRGVSAYLSRPSDFLFIKSPITICLVLDLAPSKGTVNLVTSRASGKPVNHST 180  
 QY 181 RKEEKQKNGTLTVSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKLPKRLAPEVY 240  
 Db 181 RKEEKQKNGTLTVSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKLPKRLAPEVY 240  
 QY 241 MLPPSPETGTTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKOCHGTDPSPFL 300  
 Db 241 MLPPSPETGTTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKOCHGTDPSPFL 300  
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

## RESULT 2

US-10-176-664-8  
 ; Sequence 8, Application US/10176664  
 ; Publication No. US20030031663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hellman, Lars T.  
 ; TITLE OF INVENTION: ENHANCED VACCINES  
 ; FILE REFERENCE: 10223/006001  
 ; CURRENT APPLICATION NUMBER: US/10/176,664  
 ; CURRENT FILING DATE: 2002-06-19  
 ; PRIOR APPLICATION NUMBER: US/09/401,636  
 ; PRIOR FILING DATE: 1999-09-22  
 ; PRIOR APPLICATION NUMBER: US 60/106,652  
 ; PRIOR FILING DATE: 1998-11-02  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 342  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetically generated proteins  
 US-10-176-664-8

Query Match 100.0%; Score 1856; DB 14; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-139;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
 Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
 QY 61 LVDQGAENLFPYTTTRPKREGGQTFSLQSEVNTQGMSSNTYTCVHKHNGSIFEDSSR 120  
 Db 61 LVDQGAENLFPYTTTRPKREGGQTFSLQSEVNTQGMSSNTYTCVHKHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAYLSRPSDFLFIKSPITICLVLDLAPSKGTVNLVTSRASGKPVNHST 180  
 Db 121 KCADSNPRGVSAYLSRPSDFLFIKSPITICLVLDLAPSKGTVNLVTSRASGKPVNHST 180  
 QY 181 RKEEKQKNGTLTVSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKLPKRLAPEVY 240  
 Db 181 RKEEKQKNGTLTVSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKLPKRLAPEVY 240  
 QY 241 MLPPSPETGTTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKOCHGTDPSPFL 300  
 Db 241 MLPPSPETGTTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKOCHGTDPSPFL 300  
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

## RESULT 3

US-10-673-594-8  
 ; Sequence 8, Application US/10673594  
 ; Publication No. US20040076625A1  
 ; GENERAL INFORMATION:

; APPLICANT: Hellman, Lars T.  
 ; TITLE OF INVENTION: ENHANCED VACCINES  
 ; FILE REFERENCE: 10223/006001  
 ; CURRENT APPLICATION NUMBER: US/10/673,594  
 ; CURRENT FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: US/09/401,636  
 ; PRIOR FILING DATE: 1999-09-22  
 ; PRIOR APPLICATION NUMBER: US 60/106,652  
 ; PRIOR FILING DATE: 1998-11-02  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 342  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetically generated proteins  
 US-10-673-594-8

Query Match 100.0%; Score 1856; DB 15; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-139;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
 Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60  
 QY 61 LVDQGAENLFPYTTTRPKREGGQTFSLQSEVNTQGMSSNTYTCVHKHNGSIFEDSSR 120  
 Db 61 LVDQGAENLFPYTTTRPKREGGQTFSLQSEVNTQGMSSNTYTCVHKHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAYLSRPSDFLFIKSPITICLVLDLAPSKGTVNLVTSRASGKPVNHST 180  
 Db 121 KCADSNPRGVSAYLSRPSDFLFIKSPITICLVLDLAPSKGTVNLVTSRASGKPVNHST 180  
 QY 181 RKEEKQKNGTLTVSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKLPKRLAPEVY 240  
 Db 181 RKEEKQKNGTLTVSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKLPKRLAPEVY 240  
 QY 241 MLPPSPETGTTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKOCHGTDPSPFL 300  
 Db 241 MLPPSPETGTTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKOCHGTDPSPFL 300  
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

## RESULT 4

US-10-438-794-6  
 ; Sequence 6, Application US/10438794  
 ; Publication No. US20040038395A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LUNDGREN, Mats  
 ; APPLICANT: FUENTES, Alexis  
 ; APPLICANT: MAGNUSSON, Ann-Christin  
 ; TITLE OF INVENTION: Chimeric ige Polypeptides and Host Cells  
 ; FILE REFERENCE: 10223-017001  
 ; CURRENT APPLICATION NUMBER: US/10/438,794  
 ; CURRENT FILING DATE: 2003-05-15  
 ; PRIOR APPLICATION NUMBER: US 60/382,552  
 ; PRIOR FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic polypeptide designated OSO  
 US-10-438-794-6

Query Match

96.2%; Score 1786; DB 15; Length 338;

```
Best Local Similarity 99.4%; Pred. No. 5.7e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLFPPYTRPKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRKCADSNPR 128
DB 63 NLFPPYTRPKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRKCADSNPR 122
QY 129 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSGVTNLTWSRASKGPNVHSTRKEEKOR 188
DB 123 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSGVTNLTWSRASKGPNVHSTRKEEKOR 182
QY 189 GTLTVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 183 GTLTVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKLSPGKRLAPEVYMLPPSP 242
QY 247 EETGTRTIVTCLIRGVPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLMV 306
DB 243 EETGTRTIVTCLIRGVPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLMV 302
QY 307 NKSIWEKGNLVTGRCVVEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEKGNLVTGRCVVEALPGSRTLEKSLHYSAGN 338

RESULT 5
US-10-453-915-6
; Sequence 6, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Asa
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-6

Query Match 96.2%; Score 1786; DB 15; Length 338;
Best Local Similarity 99.4%; Pred. No. 5.7e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLFPPYTRPKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRKCADSNPR 128
DB 63 NLFPPYTRPKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRKCADSNPR 122
QY 129 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSGVTNLTWSRASKGPNVHSTRKEEKOR 188
DB 123 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSGVTNLTWSRASKGPNVHSTRKEEKOR 182
QY 189 GTLTVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 183 GTLTVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKLSPGKRLAPEVYMLPPSP 242
QY 247 EETGTRTIVTCLIRGVPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLMV 306
DB 243 EETGTRTIVTCLIRGVPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLMV 302
QY 307 NKSIWEKGNLVTGRCVVEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEKGNLVTGRCVVEALPGSRTLEKSLHYSAGN 338

RESULT 6
US-10-438-794-14
; Sequence 14, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSON, Ann-Christin
; TITLE OF INVENTION: Chimeric IGE Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated OSO-H
US-10-438-794-14

Query Match 96.2%; Score 1786; DB 15; Length 347;
Best Local Similarity 99.4%; Pred. No. 5.9e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLFPPYTRPKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRKCADSNPR 128
DB 63 NLFPPYTRPKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRKCADSNPR 122
QY 129 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSGVTNLTWSRASKGPNVHSTRKEEKOR 188
DB 123 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSGVTNLTWSRASKGPNVHSTRKEEKOR 182
QY 189 GTLTVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 183 GTLTVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKLSPGKRLAPEVYMLPPSP 242
QY 247 EETGTRTIVTCLIRGVPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLMV 306
DB 243 EETGTRTIVTCLIRGVPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLMV 302
QY 307 NKSIWEKGNLVTGRCVVEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEKGNLVTGRCVVEALPGSRTLEKSLHYSAGN 338

RESULT 7
US-10-453-915-14
; Sequence 14, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Asa
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
```

```

; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-14

Query Match          96.2%; Score 1786; DB 15; Length 347;
Best Local Similarity 99.4%; Pred. No. 5.9e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 62

QY 69 NLPFYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 128
DB 63 NLPFYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 122

QY 129 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 188
DB 123 GVSAYLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 182

QY 189 GTLVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 183 GTLVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTKLASPKRLAPEVYMLPPSP 242

QY 247 EETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 306
DB 243 EETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 302

QY 307 NKSIWEGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEGNLVTCRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 8
US-10-438-794-12
; Sequence 12, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated modOSO
US-10-438-794-12

Query Match          95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 69
DB 225 IDIPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 284

QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 129
DB 285 LFPYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 344

QY 130 VSAVLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 189
DB 345 VSAVLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 404

QY 190 TLTVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 249
DB 405 TLTVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVYMLPPSP 464

QY 250 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 309
DB 465 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

```

```

QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 129
DB 285 LFPYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 344

QY 130 VSAVLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 189
DB 345 VSAVLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 404

QY 190 TLTVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 249
DB 405 TLTVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVYMLPPSP 464

QY 250 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 309
DB 465 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 9
US-10-438-794-16
; Sequence 16, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated OSO
US-10-438-794-16

Query Match          95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 69
DB 225 IDIPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 284

QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 129
DB 285 LFPYTRPKREGGQTFSLQSEVNITQGMWSSNTYCHVKHNGSIFEDSSRKCADSNPR 344

QY 130 VSAVLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 189
DB 345 VSAVLSRSPSPDLFIRKSPITICLVVDLAPSKGTNLTWSRASKGPKVNHSTRKEEKQRN 404

QY 190 TLTVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 249
DB 405 TLTVTSTLPVGRDWIEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVYMLPPSP 464

QY 250 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 309
DB 465 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLMV 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

```



```
RESULT 10
US-10-453-915-12
; Sequence 12, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Aea
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-12

Query Match      95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 69
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 284
Qy 70 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 129
Db 285 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 344
Qy 130 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 189
Db 345 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 404
Qy 190 TLTVTSTLPVGRDWEIGETQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249
Db 405 TLTVTSTLPVGRDWEIGETQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464
Qy 250 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSFFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSFFLYSRMLVNKS 524
Qy 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 11
US-10-453-915-16
; Sequence 16, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Aea
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated mcdososo-H
US-10-438-794-10

Query Match      95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 69
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 284
Qy 70 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 129
Db 285 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 344
Qy 130 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 189
Db 345 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 404
Qy 190 TLTVTSTLPVGRDWEIGETQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249
Db 405 TLTVTSTLPVGRDWEIGETQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464
Qy 250 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSFFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSFFLYSRMLVNKS 524
Qy 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-16

Query Match      95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 69
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 284
Qy 70 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 129
Db 285 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 344
Qy 130 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 189
Db 345 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 404
Qy 190 TLTVTSTLPVGRDWEIGETQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249
Db 405 TLTVTSTLPVGRDWEIGETQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464
Qy 250 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSFFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSFFLYSRMLVNKS 524
Qy 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 12
US-10-438-794-10
; Sequence 10, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated mcdososo-H
US-10-438-794-10

Query Match      95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 69
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVGQEAEN 284
Qy 70 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 129
Db 285 LPYTRPRKREGGQTFSLQSEVNITQGWMSNTYTCVHKNGSIFEDSSRKCADSNPRG 344
Qy 130 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 189
Db 345 VSAVLSRSPFDLFIKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNG 404
```

QY 190 TLTVSTLPLVGRDWEIETGYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249  
Db 405 TLTVSTLPLVGRDWEIETGYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464  
QY 250 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHHTTTRPKDGHGTDPSFFLYSRMLVNKS 309  
Db 465 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHHTTTRPKDGHGTDPSFFLYSRMLVNKS 524  
QY 310 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342  
Db 525 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 557

## RESULT 13

US-10-438-794-18  
; Sequence 18, Application US/10438794  
; Publication No. US20040038395A1  
; GENERAL INFORMATION:  
; APPLICANT: LUNDGREN, Mats  
; APPLICANT: FUENTES, Alexis  
; APPLICANT: MAGNUSSON, Ann-Christin  
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells  
; FILE REFERENCE: 10223-017001  
; CURRENT APPLICATION NUMBER: US/10/438,794  
; CURRENT FILING DATE: 2003-05-15  
; PRIOR APPLICATION NUMBER: US 60/382,552  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 566  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic polypeptide designated OSO50-H  
US-10-438-794-18

Query Match 95.5%; Score 1772; DB 15; Length 566;  
Best Local Similarity 98.5%; Pred. No. 1.4e-132;  
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTWLVGQEAEN 69  
Db 225 IDIPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTWLVGQEAEN 284  
QY 70 LPYTRPRKREGGQTFSLQSEVNIITQGMSSNTVTCVHKNGSIFEDSSRKCADSNPRG 129  
Db 285 LPYTRPRKREGGQTFSLQSEVNIITQGMSSNTVTCVHKNGSIFEDSSRKCADSNPRG 344  
QY 130 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQNG 189  
Db 345 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQNG 404  
QY 190 TLTVSTLPLVGRDWEIETGYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249  
Db 405 TLTVSTLPLVGRDWEIETGYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464  
QY 250 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHHTTTRPKDGHGTDPSFFLYSRMLVNKS 309  
Db 465 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHHTTTRPKDGHGTDPSFFLYSRMLVNKS 524  
QY 310 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342  
Db 525 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 557

## RESULT 14

US-10-453-915-10  
; Sequence 10, Application US/10453915  
; Publication No. US20040054146A1  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.

; APPLICANT: Persson, Stefan  
; APPLICANT: Jansson, Asa  
; TITLE OF INVENTION: Allergy Vaccines  
; FILE REFERENCE: 10223-008001  
; CURRENT APPLICATION NUMBER: US/10/453,915  
; CURRENT FILING DATE: 2003-06-02  
; PRIOR APPLICATION NUMBER: 60/408,648  
; PRIOR FILING DATE: 2002-09-05  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 566  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric polypeptide  
US-10-453-915-10

Query Match 95.5%; Score 1772; DB 15; Length 566;  
Best Local Similarity 98.5%; Pred. No. 1.4e-132;  
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTWLVGQEAEN 69  
Db 225 IDIPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTWLVGQEAEN 284  
QY 70 LPYTRPRKREGGQTFSLQSEVNIITQGMSSNTVTCVHKNGSIFEDSSRKCADSNPRG 129  
Db 285 LPYTRPRKREGGQTFSLQSEVNIITQGMSSNTVTCVHKNGSIFEDSSRKCADSNPRG 344  
QY 130 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQNG 189  
Db 345 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQNG 404  
QY 190 TLTVSTLPLVGRDWEIETGYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249  
Db 405 TLTVSTLPLVGRDWEIETGYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464  
QY 250 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHHTTTRPKDGHGTDPSFFLYSRMLVNKS 309  
Db 465 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHHTTTRPKDGHGTDPSFFLYSRMLVNKS 524  
QY 310 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342  
Db 525 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 557

## RESULT 15

US-10-453-915-18  
; Sequence 18, Application US/10453915  
; Publication No. US20040054146A1  
; GENERAL INFORMATION:  
; APPLICANT: Persson, Stefan  
; APPLICANT: Jansson, Asa  
; TITLE OF INVENTION: Allergy Vaccines  
; FILE REFERENCE: 10223-008001  
; CURRENT APPLICATION NUMBER: US/10/453,915  
; CURRENT FILING DATE: 2003-06-02  
; PRIOR APPLICATION NUMBER: 60/408,648  
; PRIOR FILING DATE: 2002-09-05  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 566  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric polypeptide  
US-10-453-915-18

Query Match 95.5%; Score 1772; DB 15; Length 566;  
Best Local Similarity 98.5%; Pred. No. 1.4e-132;



**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 14:55:22 ; Search time 40 Seconds  
(without alignments)  
822.653 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EPHHHHTLSUPESGVTI.....HEALPGSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: Piri:\*

2: Piri:\*

3: Piri:\*

4: Piri:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038.5	56.0	428	1 EHHU	Ig epsilon chain C
2	1024.5	55.2	426	2 I36948	Ig epsilon chain C
3	767.5	41.4	429	1 EHRT	Ig epsilon chain C
4	751	40.5	388	1 EHMS	Ig epsilon chain C
5	682	36.7	548	2 S38864	Ig epsilon chain C
6	673	36.3	423	1 EHMS	Ig epsilon chain C
7	580.5	31.3	572	2 B46529	Ig y heavy chain (
8	535.5	28.9	504	2 S00390	Ig mu chain C regi
9	497.5	26.8	479	1 MHREM	Ig mu chain C regi
10	496	26.7	454	1 MHRY	Ig mu chain C regi
11	495.5	26.7	458	1 MHRB	Ig mu chain C regi
12	486.5	26.2	326	1 G2HU	Ig gamma-2 chain C
13	480.5	25.9	343	2 S25644	Ig mu chain C regi
14	476	25.6	327	1 G4HU	Ig gamma-4 chain C
15	475.5	25.6	627	2 S14683	Ig mu chain precur
16	473.5	25.5	328	2 I47161	Ig gamma 3 chain c
17	472	25.4	433	2 S31436	Ig upsilon chain -
18	469	25.3	455	1 MHMS	Ig mu chain C regi
19	469	25.3	455	2 A24976	Ig mu chain C regi
20	469	25.3	476	1 MHMS	Ig mu chain C regi
21	468	25.2	328	2 I47160	Ig gamma 2b chain
22	465	25.1	328	2 I47159	Ig gamma 2a chain
23	465	25.1	453	2 S37768	Ig mu chain C regi
24	465	25.1	474	2 S15590	Ig heavy chain - h
25	463.5	25.0	328	2 I47158	Ig gamma 1 chain c
26	460	24.8	391	1 MHUUBT	Ig mu heavy chain
27	458.5	24.7	592	2 S25705	Ig mu chain - shee
28	454	24.5	330	1 GHU	Ig gamma-1 chain C
29	453.5	24.4	452	1 MHU	Ig mu chain C regi

30	453.5	24.4	473	1 MHUUM	Ig mu chain C regi
31	450	24.2	457	2 S03961	Ig mu chain C regi
32	447	24.1	277	2 I47182	Ig gamma 4 chain C
33	447	24.1	377	2 A23511	Ig gamma-3 chain C
34	447	24.1	377	2 A60764	Ig gamma-3 chain C
35	446.5	24.1	374	2 S69339	Ig heavy chain V r
36	444	23.9	450	1 MHDG	Ig mu chain C regi
37	443.5	23.9	322	2 PS0019	Ig gamma-2a chain
38	440	23.7	472	2 S31459	Ig gamma-1 chain -
39	437.5	23.6	323	1 GHRB	Ig gamma chain C r
40	437.5	23.6	444	2 PC4436	monoclonal antibod
41	436.5	23.5	326	2 PS0017	Ig gamma-1 chain C
42	429	23.1	470	2 S22080	Ig heavy chain pre
43	428	23.1	329	2 S00847	Ig gamma-2c chain
44	428	23.1	549	2 S04845	Ig heavy chain pre
45	424.5	22.9	329	1 G2GP	Ig gamma-2 chain C

#### ALIGNMENTS

##### RESULT 1

EHU

Ig epsilon chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B99393; S02438; A53116; C4

R:Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gen

A:Reference number: A22771; MUID:84236029; PMID:6234164

A:Accession: A22771

A:Molecule type: DNA

A:Residues: 1-428 <FLA>

A:Cross-references: UNIPROT:P01854; GB:L00022; GB:J00227; GB:V00555; NID:G185035

R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudo

A:Reference number: A23195; MUID:84207910; PMID:6327276

A:Accession: A23195

A:Molecule type: DNA

A:Residues: 2-428 <UED>

A:Cross-references: GB:J00222; NID:G184755

R:Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992

A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicin

A:Reference number: PH1214; MUID:92308839; PMID:1613458

A:Accession: PH1214

A:Molecule type: DNA

A:Residues: 320-428 <ZHA>

A:Cross-references: EMBL:X63693; GB:S38668; NID:G32987

R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sug

Nucleic Acids Res. 11, 719-726, 1993

A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon ch

A:Reference number: A93491; MUID:83168897; PMID:6300763

A:Accession: A93491

A:Molecule type: mRNA

A:Residues: 1-428 <SEN>

A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:G185035

R:Max, E.E.; Battery, J.; Ney, R.; Kirsch, I.R.; Leder, P.

Cell 29, 691-699, 1982

A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.

A:Reference number: A90824; MUID:83001945; PMID:6288268

A:Accession: A90824

A:Molecule type: DNA

A:Residues: 1-358, 'L', 360-428 <MAX>

A:Cross-references: GB:J00222; NID:G184755

A>Note: this sequence difference may be due to polymorphism

R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-

A:Reference number: A94418

A:Accession: A94418

A:Molecule type: protein

A;Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',141,'L',143,'L',145,'L',147,'L',149,'L',151,'L',153,'L',155,'L',157,'L',159,'L',161,'L',163,'L',165,'L',167,'L',169,'L',171,'L',173,'L',175,'L',177,'L',179,'L',181,'L',183,'L',185,'L',187,'L',189,'L',191,'L',193,'L',195,'L',197,'L',199,'L',201,'L',203,'L',205,'L',207,'L',209,'L',211,'L',213,'L',215,'L',217,'L',219,'L',221,'L',223,'L',225,'L',227,'L',229,'L',231,'L',233,'L',235,'L',237,'L',239,'L',241,'L',243,'L',245,'L',247,'L',249,'L',251,'L',253,'L',255,'L',257,'L',259,'L',261,'L',263,'L',265,'L',267,'L',269,'L',271,'L',273,'L',275,'L',277,'L',279,'L',281,'L',283,'L',285,'L',287,'L',289,'L',291,'L',293,'L',295,'L',297,'L',299,'L',301,'L',303,'L',305,'L',307,'L',309,'L',311,'L',313,'L',315,'L',317,'L',319,'L',321,'L',323,'L',325,'L',327,'L',329,'L',331,'L',333,'L',335,'L',337,'L',339,'L',341,'L',343,'L',345,'L',347,'L',349,'L',351,'L',353,'L',355,'L',357,'L',359,'L',361,'L',363,'L',365,'L',367,'L',369,'L',371,'L',373,'L',375,'L',377,'L',379,'L',381,'L',383,'L',385,'L',387,'L',389,'L',391,'L',393,'L',395,'L',397,'L',399,'L',401,'L',403,'L',405,'L',407,'L',409,'L',411,'L',413,'L',415,'L',417,'L',419,'L',421,'L',423,'L',425,'L',427,'L',429,'L',431,'L',433,'L',435,'L',437,'L',439,'L',441,'L',443,'L',445,'L',447,'L',449,'L',451,'L',453,'L',455,'L',457,'L',459,'L',461,'L',463,'L',465,'L',467,'L',469,'L',471,'L',473,'L',475,'L',477,'L',479,'L',481,'L',483,'L',485,'L',487,'L',489,'L',491,'L',493,'L',495,'L',497,'L',499,'L',501,'L',503,'L',505,'L',507,'L',509,'L',511,'L',513,'L',515,'L',517,'L',519,'L',521,'L',523,'L',525,'L',527,'L',529,'L',531,'L',533,'L',535,'L',537,'L',539,'L',541,'L',543,'L',545,'L',547,'L',549,'L',551,'L',553,'L',555,'L',557,'L',559,'L',561,'L',563,'L',565,'L',567,'L',569,'L',571,'L',573,'L',575,'L',577,'L',579,'L',581,'L',583,'L',585,'L',587,'L',589,'L',591,'L',593,'L',595,'L',597,'L',599,'L',601,'L',603,'L',605,'L',607,'L',609,'L',611,'L',613,'L',615,'L',617,'L',619,'L',621,'L',623,'L',625,'L',627,'L',629,'L',631,'L',633,'L',635,'L',637,'L',639,'L',641,'L',643,'L',645,'L',647,'L',649,'L',651,'L',653,'L',655,'L',657,'L',659,'L',661,'L',663,'L',665,'L',667,'L',669,'L',671,'L',673,'L',675,'L',677,'L',679,'L',681,'L',683,'L',685,'L',687,'L',689,'L',691,'L',693,'L',695,'L',697,'L',699,'L',701,'L',703,'L',705,'L',707,'L',709,'L',711,'L',713,'L',715,'L',717,'L',719,'L',721,'L',723,'L',725,'L',727,'L',729,'L',731,'L',733,'L',735,'L',737,'L',739,'L',741,'L',743,'L',745,'L',747,'L',749,'L',751,'L',753,'L',755,'L',757,'L',759,'L',761,'L',763,'L',765,'L',767,'L',769,'L',771,'L',773,'L',775,'L',777,'L',779,'L',781,'L',783,'L',785,'L',787,'L',789,'L',791,'L',793,'L',795,'L',797,'L',799,'L',801,'L',803,'L',805,'L',807,'L',809,'L',811,'L',813,'L',815,'L',817,'L',819,'L',821,'L',823,'L',825,'L',827,'L',829,'L',831,'L',833,'L',835,'L',837,'L',839,'L',841,'L',843,'L',845,'L',847,'L',849,'L',851,'L',853,'L',855,'L',857,'L',859,'L',861,'L',863,'L',865,'L',867,'L',869,'L',871,'L',873,'L',875,'L',877,'L',879,'L',881,'L',883,'L',885,'L',887,'L',889,'L',891,'L',893,'L',895,'L',897,'L',899,'L',901,'L',903,'L',905,'L',907,'L',909,'L',911,'L',913,'L',915,'L',917,'L',919,'L',921,'L',923,'L',925,'L',927,'L',929,'L',931,'L',933,'L',935,'L',937,'L',939,'L',941,'L',943,'L',945,'L',947,'L',949,'L',951,'L',953,'L',955,'L',957,'L',959,'L',961,'L',963,'L',965,'L',967,'L',969,'L',971,'L',973,'L',975,'L',977,'L',979,'L',981,'L',983,'L',985,'L',987,'L',989,'L',991,'L',993,'L',995,'L',997,'L',999,'L',1001,'L',1003,'L',1005,'L',1007,'L',1009,'L',1011,'L',1013,'L',1015,'L',1017,'L',1019,'L',1021,'L',1023,'L',1025,'L',1027,'L',1029,'L',1031,'L',1033,'L',1035,'L',1037,'L',1039,'L',1041,'L',1043,'L',1045,'L',1047,'L',1049,'L',1051,'L',1053,'L',1055,'L',1057,'L',1059,'L',1061,'L',1063,'L',1065,'L',1067,'L',1069,'L',1071,'L',1073,'L',1075,'L',1077,'L',1079,'L',1081,'L',1083,'L',1085,'L',1087,'L',1089,'L',1091,'L',1093,'L',1095,'L',1097,'L',1099,'L',1101,'L',1103,'L',1105,'L',1107,'L',1109,'L',1111,'L',1113,'L',1115,'L',1117,'L',1119,'L',1121,'L',1123,'L',1125,'L',1127,'L',1129,'L',1131,'L',1133,'L',1135,'L',1137,'L',1139,'L',1141,'L',1143,'L',1145,'L',1147,'L',1149,'L',1151,'L',1153,'L',1155,'L',1157,'L',1159,'L',1161,'L',1163,'L',1165,'L',1167,'L',1169,'L',1171,'L',1173,'L',1175,'L',1177,'L',1179,'L',1181,'L',1183,'L',1185,'L',1187,'L',1189,'L',1191,'L',1193,'L',1195,'L',1197,'L',1199,'L',1201,'L',1203,'L',1205,'L',1207,'L',1209,'L',1211,'L',1213,'L',1215,'L',1217,'L',1219,'L',1221,'L',1223,'L',1225,'L',1227,'L',1229,'L',1231,'L',1233,'L',1235,'L',1237,'L',1239,'L',1241,'L',1243,'L',1245,'L',1247,'L',1249,'L',1251,'L',1253,'L',1255,'L',1257,'L',1259,'L',1261,'L',1263,'L',1265,'L',1267,'L',1269,'L',1271,'L',1273,'L',1275,'L',1277,'L',1279,'L',1281,'L',1283,'L',1285,'L',1287,'L',1289,'L',1291,'L',1293,'L',1295,'L',1297,'L',1299,'L',1301,'L',1303,'L',1305,'L',1307,'L',1309,'L',1311,'L',1313,'L',1315,'L',1317,'L',1319,'L',1321,'L',1323,'L',1325,'L',1327,'L',1329,'L',1331,'L',1333,'L',1335,'L',1337,'L',1339,'L',1341,'L',1343,'L',1345,'L',1347,'L',1349,'L',1351,'L',1353,'L',1355,'L',1357,'L',1359,'L',1361,'L',1363,'L',1365,'L',1367,'L',1369,'L',1371,'L',1373,'L',1375,'L',1377,'L',1379,'L',1381,'L',1383,'L',1385,'L',1387,'L',1389,'L',1391,'L',1393,'L',1395,'L',1397,'L',1399,'L',1401,'L',1403,'L',1405,'L',1407,'L',1409,'L',1411,'L',1413,'L',1

Db 405 AVHEAAPSQTVORTVSVNPG 425

## RESULT 3

EHRT

Ig epsilon chain C region - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 17-Dec-1992 #sequence\_revision 17-Dec-1982 #text\_change 09-Jul-2004  
C:Accession: A93442; A90937; A02143  
R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.  
Nucleic Acids Res. 10, 6041-6049, 1982  
A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.  
A:Reference number: A93442; MUID:83064537; PMID:6292865  
A:Accession: A93442  
A:Molecule type: mRNA  
A:Residues: 1-429 <HEL>  
A:Cross-references: UNIPROT:P01855  
A:Experimental source: strain LOU/c/Wsl, immunocytoma IR2  
R:Kindavogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.  
DNA 1, 335-343, 1982  
A:Title: A cloned cDNA probe for rat immunoglobulin epsilon chain: construction, i  
A:Reference number: A90937; MUID:83182019; PMID:6820340  
A:Contents: myeloma IR162  
A:Accession: A90937  
A:Molecule type: mRNA  
A:Residues: 'N', 169-307, 'L', 309-342 <KIN>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:19-80/Domain: immunoglobulin homology <IM1>  
F:118-186/Domain: immunoglobulin homology <IM2>  
F:223-291/Domain: immunoglobulin homology <IM3>  
F:327-398/Domain: immunoglobulin homology <IM4>  
F:45,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 41.4%; Score 767.5; DB 1; Length 429;  
Best Local Similarity 45.8%; Pred. No. 1.1e-49;  
Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;  
QY 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFPAKVHTWLVGDGEAENLPPYTR 76  
Db PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFPAKVHTWLVGDGEAENLPPYTR 76  
QY 77 PK---REGQTFSLQSEVNITQGMSSNTYTCVHKGNSIPEDSSRKCADSNPRGVA 132  
Db AQNVLKEGKLASTVSLRNITQQMWSBSTFCKVTSGENYWAHTRCSDDEPRGVIT 210  
QY 133 YLSPGPFDFIRKSPITICLVVDLAPSKGTWNLTSRAGKPVNHSRKEKQKQNGTLT 192  
Db YLIPPSPLDLYENGTEPKLTCLVLDL-ESSENITVTVWRERKKSIGSASQSRKHNATTS 269  
QY 193 VTSTLPVGRDWTGEGTYQCRVTHPLPRALVRSTTKLPKGLAPRVNMLPPSPETGTT 252  
Db ITSILPDAKDWLEGYQCRVDHPFPKPIVRSITKAFKGSAPVYVFLPPEEEKDK 329  
QY 253 RVTCTIIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGDTDPSPFLYSRMLVNKSIWE 312  
Db RTLTCLIQNFPPEDISVQWLDKSLPKSGHSTTTTLKYNQSGNORPFISRLVTKALWT 389  
QY 313 KGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342  
Db QTQKQTCRVVHEALREPRKLTERTISKSUN 419

## RESULT 4

EHMS

Ig epsilon chain C region (version 1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
C:Accession: A02144  
R:Liou, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.  
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.  
A:Reference number: A02144; MUID:83117774; PMID:6818553  
A:Accession: A02144  
A:Molecule type: mRNA  
A:Residues: 1-388 <LIU>  
A:Cross-references: UNIPROT:P06336; GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g38722  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:1-44/Domain: immunoglobulin homology (fragment) <IM1>  
F:61-149/Domain: immunoglobulin homology <IM2>  
F:186-254/Domain: immunoglobulin homology <IM3>  
F:290-361/Domain: immunoglobulin homology <IM4>  
F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 40.5%; Score 751; DB 1; Length 388;  
Best Local Similarity 44.8%; Pred. No. 1.7e-48;  
Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;  
QY 2 FHHHHHTLSLPES-----GPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFPAKV 56  
Db F186-254/Domain: immunoglobulin homology <IM3>  
QY 57 HVTWLVGDGEAENLPPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKGNSIFE 116  
Db SVSLMDDREITDILAQVLIKEE-GKLAETCSKLNITEQQMSESTFTCKVTSGVDYL 157  
QY 117 DSSRKCADSNPRGVSAYLSRSPDFDFIRKSPITICLVVDLAPSKGTWNLTSRAGKPV 176  
Db ATRRCRCPDHPRGVITYLIPSPDLVQNGAPKLTCLVVDLESEK-NVNVITWNOEKTSV 216  
QY 177 NHRTRKEKQKQNGTLTWTSTLPVGRDWTGEGTYQCRVTHPLPRALVRSTTKLPKGLA 236  
Db SASQWYTKHNNATTSITSLPVVAKQWIEGYQCTVDPDFPKPIVRSITKTPGQSA 276  
QY 237 PEVYMLPPSPETGTRTTCVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGDTDP 296  
Db PEVYVFPPEBESDKRTLCILQNFPPEDISVQWLDGKLSNSQHSSTTTPKLSNSNQ 336  
QY 297 SFYYSRMLVNKSIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342  
Db GFFIFSRLEAVLTWTKQTCQVHEALQKPRKLEKTISTSLGN 382

## RESULT 5

S38864

Ig epsilon chain C region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001  
C:Accession: S38864  
R:Kipp, B.; Becker, W.; Schlaak, W.  
submitted to the EMBL Data Library, November 1993  
A:Description: Combination of a defined specificity and desired isotype by cloning of a  
A:Reference number: S38864  
A:Accession: S38864  
A:Molecule type: mRNA  
A:Residues: 1-548 <KIP>  
A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:353-421/Domain: immunoglobulin homology <IMV>

Query Match 36.7%; Score 682; DB 2; Length 548;  
Best Local Similarity 43.0%; Pred. No. 3.6e-43;  
Matches 142; Conservative 52; Mismatches 122; Indels 14; Gaps 4;

QY 12 LPESGPVTIIPPTVKLFHSSCDPRGD--AHSTIQLCLVSGFPAKVHTWLVGDQAEEN 69  
Db VPEVSSVFIFFPKPK-----DVLTRSTIQLCYCFIYGHILNDVSVSLMDDREITD 278  
QY 70 LPFYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKGNSIFEDSSRKCADSNPRG 129

Db 279 TLAQTVLKEE-GKLASTCKLNITEQWSESTFTCKVTSGVDYLAHTRCPDHEPRG 337  
 QY 130 VSAIYLRSPDFLPIKSTITCLVLDLAPSGVTNLTWSRSGKPVVHSTRKEKQNG 189  
 Db 338 VITYLIPSPDLQYNGAPKLTCLVLDLESEK-VNVTWNQSKTSVSAQWYTKHNA 396  
 QY 190 TLVTITLPLVGTDMTEGYTCQVTHPHLPALMRSTTKLPKRLAPEVYMLPSPSET 249  
 Db 397 TTSITSLPVAKDWIEGYQYQIVDHPDFPKPIVRSITKTQGSAPVYVFPPEES 456  
 QY 250 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRQKDHGTDPSFFLYSRMLVNS 309  
 Db 457 EDKRTITCLIQNFPFEDISVQWLDGKLSNQSHSTTTPLKSGNSRNGRFFIFSRLEAVT 516  
 QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHVS 339  
 Db 517 LWTQRQKTCQVTHEALQPKRLEKTIIST 546

RESULT 6  
 ERMSS  
 Ig epsilon chain C region (version 2) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
 C:Accession: A02145  
 R:Ushida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.  
 EMBO J. 1, 1117-1123, 1982  
 A:Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with human epsilon gene  
 A:Reference number: A90966; MUID:84236092; PMID:6329728  
 A:Accession: A02145  
 A:Molecule type: DNA  
 A:Residues: 1-423 <ISH>  
 A:Cross-references: UNIPROT:P06336  
 A:Note: the sequence was determined from the germline gene  
 C:Genetics:  
 A:Introns: 91/1: 199/1: 307/1  
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:16-77/Domain: immunoglobulin homology <IMM1>  
 F:115-183/Domain: immunoglobulin homology <IMM2>  
 F:220-288/Domain: immunoglobulin homology <IMM3>  
 F:325-396/Domain: immunoglobulin homology <IMM4>  
 F:23-75,122-181,227-286,332-394/disulfide bonds: #status predicted  
 F:43,84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.3%; Score 673; DB 1; Length 423;  
 Best Local Similarity 41.6%; Pred. No. 1.2e-42;  
 Matches 147; Conservative 53; Mismatches 133; Indels 20; Gaps 7;

QY 2 FHHHHHTLSLPESGVTPIPTPVKLFHS-----SCDPRGDAHSTIQLCLVSGF 51  
 Db 73 FTCHVTTHPSFNESRTILVRPVT---HSLSPWMSYIHRCPDFA-FHSTIQLYCFIYGH 127  
 QY 52 SPAKVHVTMLVDQEAENLPPYTRPRKGGQTFSLQSEVNITQGWMSNTYTCVVKHN 111  
 Db 128 ILNDVSWSLMDREITDLAQVLKEE-GKLASTCKLNITEQWSESTFTCRVTSQ 186  
 QY 112 GSIFEDSSRKACDNRPGVSAIYLRSPDFDLPIKSTITCLVLDLAPSGVTNLTWSR 171  
 Db 187 GVDYLAHTRCPDHEPRGAIITLIPSPDLQYNGAPKLTCLVLDLESEK-VNVTWNQ 245  
 QY 172 SGKPVNHSFRKEKQKNGTLTSTVPGTRDWIEGETYQCRVTHPHLPALMRSTTKLP 231  
 Db 246 KTSVSAQWYTKHNNATISILPVAKDWIEGYQYQIVDHPDFPKPIVRSIT-LP 304  
 QY 232 --GKRLAPEVYMLPSPSETGTTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPQ 289  
 Db 305 QVSGRAPEVYVFPPEESEDKRTITCLIQNFPFEDISVQWLDGKLSNQSHSTTTPL 364  
 QY 290 KDHGTDPSFFLYSRMLVNSIWEKGNLVTCTRVVHEALPGSRTLEKSLHVSACN 342

Db 365 KSGNSQGFIFSRLEAVTWTQRQKTCQVTHEALQPKRLEKTIISTSLGN 417

RESULT 7  
 B46529  
 Ig Y heavy chain (7.8S) - duck  
 N:Alternate names: Ig gamma chain (7.8S)  
 C:Species: Anas platyrhynchos (domestic duck)  
 C>Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
 C:Accession: B46529; S20759  
 R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.  
 J. Immunol. 149, 2627-2633, 1992  
 A:Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos: molecular cloning and sequencing of the heavy chain genes  
 A:Reference number: A46529; MUID:93017865; PMID:1401901  
 A:Accession: B46529  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-572 <MAG>  
 A:Cross-references: EMBL:X65219; NID:962442; PIDN:CAA46322.1; PID:962443  
 A:Experimental source: spleen  
 A:Note: sequence extracted from NCBI backbone (NCBIP:116127)  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 580.5; DB 2; Length 572;  
 Best Local Similarity 38.2%; Pred. No. 1.4e-35;  
 Matches 124; Conservative 56; Mismatches 130; Indels 15; Gaps 9;

QY 22 PPTVKLFHSS-CDPRGDAHSTIQLCLVSGFSAPKVVHVTMLVDQEAENLFPYTRPKRE 80  
 Db 249 PPEVQLHSSVCSTLGD--DSVELLCVITGFSPPPEVEWLVGDGAP-HLVAMTRPQRE 305  
 QY 81 -GGQTFSLQSEVNITQGWMSNTYTCVVKH--NGSIFEDSSRKACDNRPG--VSAVL 134  
 Db 306 AGSKTYMATSGTNSREDWAKGAKTCRVKHPATGTAQGHAFRCFSGAQCSPQIFV 365  
 QY 135 SRSPDFLPIKSTITCLVLDLAPSGVTNLTWSRSGKPVVHSTRKEKQKNGTLT 194  
 Db 366 VPSPGGLYIRQDAKVHCLLVNL-PSDASLSISWTREKSGALRPDPMLVTEHNGFTTAS 424  
 QY 195 STLFPVGTDRWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPSPSETGTT 253  
 Db 425 SSLAISTQDMLAGERFTCTVQHEDLVPVLGKSIAGKAVTAPYIETFPFHASELSLA 484  
 QY 254 TVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPQKDHGTDPSFFLYSRMLVNSIWEK 313  
 Db 485 TLTCVREGFOPEHVEVQWLNHNNSVPAAEFVTPPPLKEPNNGDGTFFLYSKVTVPKAS 544  
 QY 314 GNLVTCRWVHEALP--GSRTLEKS 335  
 Db 545 GVSACVWVHEGLPMRFTQRPLOKT 569

RESULT 8  
 S00390  
 Ig gamma chain (clone 36) - chicken (fragment)  
 N:Alternate names: Ig nu chain  
 C:Species: Gallus gallus (chicken)  
 C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 11-Jan-2000  
 C:Accession: S00390  
 R:Parvari, R.; Avivi, A.; Lenthner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, I.  
 EMBO J. 7, 739-744, 1988  
 A:Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combination of D and J segments, and the presence of a D-J join  
 A:Reference number: S00390; MUID:88283642; PMID:3135182  
 A:Accession: S00390  
 A:Molecule type: mRNA  
 A:Residues: 1-504 <PAR>  
 A:Cross-references: EMBL:X07174  
 A:Note: this sequence was determined from the differentiated gene  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin





Db 389 APLHYTHSVLTWTEBWSGETYTCVVGHEALPHWVTRTVDRS 433

RESULT 11

MHRB

IG mu chain C region, secreted form - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 09-Jul-2004

C:Accession: A02164

R:Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.

J. Immunol. 132, 490-495, 1984

A:Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Ha2 a

A:Reference number: A02164; MUID:84088930; PMID:6418803

A:Contents: a2 allotype

A:Accession: A02164

A:Molecule type: mRNA

A:Residues: 1-458 <BER>

A:Cross-references: UNIPROT:P03988

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu

F:11-32/Domain: immunoglobulin homology <IM1>

F:130-202/Domain: immunoglobulin homology <IM2>

F:242-310/Domain: immunoglobulin homology <IM3>

F:349-420/Domain: immunoglobulin homology <IM4>

F:14/Disulfide bonds: interchain (to light chain) #status predicted

F:28-90,137-249,308,356-418/Disulfide bonds: #status predicted

F:46,114,212,261,277,284,445/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:219,457/Disulfide bonds: interchain (to heavy chain) #status predicted

F:236/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.7%; Score 495.5; DB 1; Length 458;

Best Local Similarity 33.1%; Pred. No. 2.2e-29;

Matches 116; Conservative 61; Mismatches 148; Indels 25; Gaps 10;

QY 5 HHHTLSLPESGPV-TIIPPTVKLPHSSCDPR-----GDAHSITQLLCVSGSPAKVHVT 59

Db 94 HNSNDRLRVSPVSELPVSFV---IPPRDSFGSGTRKSLRICATGSPKQISVS 150

QY 60 WLVDGQAEEN---LFYTPTRPKREGQTESLOSEYVNIQGWSSNTVTCVKNKGSIFE 116

Db 151 WLVDGQKVESGLVTKPVEATKAGPATFSISMLTIESDWLSQSLYTCRVDHRGIFD 210

QY 117 DS---SRKCADSNPRVSAYLRSPFDFPIKSPPTICLVVDLAPSGKTNLTWSRAG 173

Db 211 KQVMSSESGCTPSPGIQVFPPIAPSPADTFLSKSARLICLVLDLT-TYGSLSNWSHNG 269

QY 174 KPVNHSTRKEEKORNGTLVTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPKG 233

Db 270 KALDTHMNTESHPNATFAMEASVCAEDWSGQPCITVTHADLPFLKHTISK--SR 327

QY 234 RLA---PEVYMLPPSPPEE--TGTRVTCCLIRGFVPSEISVQWLFNNEEDTGHHTTTP 288

Db 328 EVAKHPVAVVYLPAPAEQLVLRSAATVCLVKGFSADVFVQVQQRGQPLSSDKYVTGAP 387

QY 289 QKDHGTDTPFFLYSRMLVKNKSTWEKNLVTCRVVHEALP---GSRITLKS 335

Db 388 APEQAPQGLGYFTHSTLTVTVEEDNWSGETTTCVVGHEALPHWVTRTVDRS 437

RESULT 12

G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93132; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma chain cor

A:Reference number: A93906; MUID:82157621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:532759; PIDN:CAB58438.1; P

A:Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f

A:Reference number: A92809; MUID:81007873; PMID:6774012

A:Contents: myeloma protein Til

A:Accession: A92809

A:Molecule type: protein

A:Residues: 1-19, Q, 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>

A:Note: Trp-156 is at or near the complement-binding site

R:Connell, G.B.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; MUID:80001357; PMID:113060

A:Contents: myeloma protein Zie

A:Accession: A90752

A:Molecule type: protein

A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-

A:Note: this sequence has since been revised

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G

A:Reference number: A93132; MUID:80114419; PMID:118920

A:Contents: Zie

A:Accession: A93132

A:Molecule type: protein

A:Residues: 238-275 <HOF>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas. March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati

ned

R:Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A:Title: Structural studies of immunoglobulin G.

A:Reference number: A93157; MUID:69064124; PMID:5782707

A:Contents: annotation; Sa, disulfide bonds

C:Genetics:

A:Gene: GDB:IGH2

A:Cross-references: GDB:119338; OMIM:147110

A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.2%; Score 486.5; DB 1; Length 326;

Best Local Similarity 36.2%; Pred. No. 6.7e-29;

Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGAHSITQLLCVSGSPAKVHVTW---LVDPQAEHLFPYTTTRPKREGQTFSLQSE 90

Db 16 RSTSESTAALGCVLKDYFPFPVTVSNWSGALTSG---VHTFPAVL-----QSSGLVSLSSV 68

QY 91 VNTQGWSSNTYTCVKNK---NGSIFEDSSRKCADSNP-----RGVSAYLSRSPFP 140

Db 69 VTFPSSNF-GTQYTCNVNDHKPSNTKVDKTKVERKCCVCEPCPAPVAGSPVFLPFPKPK 127

QY 141 D-LFIRKSPITICLVVDLAPSKGTNLVTSRAGKVPVNHSTRKEEKQKRGNTLTVTSTLPV 199  
 DB 128 DTLMIKRTPEVTCVVDVSHEDDEVQFNWVDGVEVHNKAKTRPEQFNSTRFVSVLTV 187  
 QY 200 GTDWDIEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEE-TGTRTVTCL 258  
 DB 188 VHQDNLNGKEYCKVKNKGLPAPIETIKTKGQPREPQVYTLPPSREEMTKNQVSLTCL 247  
 QY 259 IRGFYPSSEISVQMLFNNEDHTGHTTTPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLV 318  
 DB 248 VKGFYPSDIAVESNGQPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRWQGNVPS 303  
 QY 319 CRVVEALPGSRITLKSLSHSAG 341  
 DB 304 CSVWHEALHNHYT-QKSLSLSPG 325

RESULT 13  
 S25644  
 Ig mu chain C region - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Feb-1995 #sequence\_revision 30-Jan-1998 #text\_change 21-Jan-2000  
 C:Accession: S25644  
 R:Parker, K.; Bugeon, L.; Soullou, J.P.  
 Submitted to the EMBL Data Library, September 1992  
 A:Reference number: S25644  
 A:Accession: S25644  
 A:Molecule type: mRNA  
 A:Residues: 1-343 <PAR>  
 A:Cross-references: EMBL:X68312; NID:G56461; PIDN:CAA48392.1; PID:G818025  
 A:Experimental source: spleen  
 C:Genetics:  
 A:Map position: 6  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:234-305/Domain: immunoglobulin homology <IMM>

Query Match 25.9%; Score 480.5; DB 2; Length 343;  
 Best Local Similarity 34.7%; Pred. No. 2e-28;  
 Matches 108; Conservative 59; Mismatches 131; Indels 13; Gaps 7;

QY 36 GDAHSTIQLCLVSGSPAKVHVTVLVDGQEAENLF---PYTRPKREGQTFSLQSEV 92  
 DB 14 GPAPKSRILCEATNESPQKITVSLQDGKPKVSGFTTEPVTAEGKSRPQYKVISLT 73  
 QY 93 ITGQGWSSNTYCHVKNGSIF-EDSRKCADSNPRGVSAVLSRPSPDLLFIRKSPIT 151  
 DB 74 ITESDNLNVFTCRVDHRLGTLFWKNVSTCAASPSDILAPIPPSFADIFLTSAKL 133  
 QY 152 CLVVDLAPSKGTNLVTSRAGKVPVNHSTRKEEKQKRGNTLTVTSTLPVGTDRWIEGTYQ 211  
 DB 134 CLVTNLA-TYDTLNISSWSKSGEPLTNTKIMESHENGTFSAVGVAVCMDNDNRKRV 192  
 QY 212 CRVTHPHLPALMRSTTKLPK--RLAPEVYMLPPSPPEE-TGTRTVTCLIRGYPSEI 267  
 DB 193 CTVTHRDLPSPQCKFISK-PNEVAKHPAPVYLLPAREQLIRESATVTLCKVGFSPADI 251  
 QY 268 SVQMLFNNEDHTGHTTTPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLVTCRVVHEALP 327  
 DB 252 FVQWLQRGQPLSDKVTYTSAPWPEPCAPGLYTHSLTITVEEWSNGEITYTCVGHREALP 311

QY 328 ---GSRTLEKS 335  
 DB 312 HMVTERTVDKS 322

RESULT 14  
G4HU

Ig gamma-4 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
 C:Accession: A90933; A90249; A02150  
 R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981.  
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
 A:Reference number: A90933; MUID:83157104; PMID:6299662  
 A:Accession: A90933  
 A:Molecule type: DNA  
 A:Residues: 1-327 <ELL>  
 A:Cross-references: UNIPROT:P01861  
 A>Note: the sequence was determined from the germline gene  
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
 Biochem. J. 117, 33-47, 1970  
 A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant  
 A:Reference number: A90249; MUID:70207560; PMID:4192699  
 A:Accession: A90249  
 A:Molecule type: protein  
 A:Residues: 1-30; 81-326 <PIN>  
 C:Genetics:  
 A:Gene: GDB:IGHG4  
 A:Cross-references: GDB:119340; OMIM:147130  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 99/1; 111/1; 221/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-95/Domain: immunoglobulin homology <IM1>  
 F:99-110/Region: hinge  
 F:134-203/Domain: immunoglobulin homology <IM2>  
 F:240-307/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
 F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 476; DB 1; Length 327;  
 Best Local Similarity 35.8%; Pred. No. 4.1e-28;  
 Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGDHSTIQLCLVSGSPAKVHVTVLVDGQEAENLFVYTRPKREGQTFSLQSE 90  
 DB 16 RSTSESTALGCLVKYDFPEPVTVMNSGALTSG---VHTFPAVL---QSSGLYSLSV 68  
 QY 91 VNITQGWSSNTYCHVKNGSIFEDSRKCADSNP-----RGVSAVLSRPS 139  
 DB 69 VTVFSS--LGKTYTCNVVDHKPSNTKVDKVESKYGPCPCAPPEFLGGPSVFLPPKP 127  
 QY 140 FD-LFIRKSPITICLVVDLAPSKGTNLVTSRAGKVPVNHSTRKEEKQKRGNTLTVTSTLP 198  
 DB 128 KDTLMISRTPEVTCVVDVSHEDDEVQFNWVDGVEVHNKAKTRPEQFNSTRFVSVLTV 187  
 QY 199 VGTDRWIEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEE-TGTRTVTC 257  
 DB 188 VLHQDNLNGKEYCKVKNKGLPSSIEKTSKAKQPREPQVYTLPPSREEMTKNQVSLTC 247  
 QY 258 LIRGFYPSSEISVQMLFNNEDHTGHTTTPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLV 317  
 DB 248 LVKGFYPSDIAVESNGQPEN--NYKTPPVLDD--SDGSFFLYSLTVDKSRWQGNV 303  
 QY 318 TCRVVEALPGSRITLKSLSHSAG 341  
 DB 304 CSVWHEALHNHYT-QKSLSLSLG 326

RESULT 15  
 S14683  
 Ig mu chain precursor, membrane-bound (clone 201) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
 R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
 Nucleic Acids Res. 18, 4278, 1990  
 A:Title: Complete nucleotide sequence of the membrane form of the human IGM heavy chain  
 A:Reference number: S14683; MUID:90332450; PMID:2115996  
 A:Accession: S14683



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 14:55:18 ; Search time 191 Seconds  
(without alignments)  
1030.252 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EFHHHHHTLSLPESGVPTL.....HEALPGSRTLESLHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:\*

1: uniprot\_prot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038.5	55.0	428	1 EPC HUMAN	P01854 homo sapien
2	1033.5	55.7	571	2 BAC85440	Bac85440 homo sapi
3	767.5	41.4	429	1 EPC RAT	P01855 rattus norv
4	761	40.5	421	1 EPC MOUSE	P06336 mus musculu
5	497.5	26.8	479	1 MUCM RABIT	P04221 oryctolagus
6	496.5	26.8	464	2 Q6MZU6	Q6mzu6 homo sapien
7	496.5	26.8	464	2 CAE45931	CAe45931 homo sapi
8	495.5	26.7	458	1 MUC RABIT	P03988 oryctolagus
9	493.5	26.6	464	2 BAC85395	Bac85395 homo sapi
10	493.5	26.6	468	2 BAC85483	Bac85483 homo sapi
11	488.5	26.3	465	2 Q6P6C4	Q6p6c4 homo sapien
12	488.5	26.3	465	2 AAH62335	AAh62335 homo sapi
13	486.5	26.2	326	1 GC2 HUMAN	AAh62335 homo sapi
14	486.5	26.2	417	2 Q6N093	Q6n093 homo sapien
15	486.5	26.2	417	2 CAE45777	CAe45777 homo sapi
16	483	26.0	454	1 MUC MSAU	P06337 mesocricetu
17	482.5	26.0	337	2 Q95W34	Q95w34 equus cabal
18	482.5	26.0	472	2 BAC85393	Bac85393 homo sapi
19	479.5	25.8	473	2 Q8TC63	Q8tc63 homo sapien
20	479.5	25.8	476	2 Q6VZX7	Q6vzx7 homo sapien
21	479.5	25.8	476	2 CAE45900	CAe45900 homo sapi
22	476	25.6	327	1 GC4 HUMAN	P01861 homo sapien
23	475.5	25.6	454	1 MUC HUMAN	P01871 homo sapien
24	470	25.3	614	2 Q7MT6	Q7mt6 mus musculu
25	469	25.3	455	1 MUC MOUSE	P01872 mus musculu
26	468	25.3	476	1 MUCM MOUSE	P01873 mus musculu
27	469	25.3	613	2 Q8VCX7	Q8vcx7 mus musculu
28	467	25.2	548	2 BAD00196	Bad00196 camelus d
29	465	25.1	375	2 Q86T11	Q86t11 homo sapien
30	465	25.1	480	2 Q6PJF1	Q6pjf1 homo sapien
31	465	25.1	480	2 AAH16381	AAh16381 homo sapi

32 465 25.1 595 2 Q8WUX4 Q8wux4 homo sapien  
33 465 25.1 597 2 Q8GMX5 Q8gmX5 homo sapien  
34 465 25.1 597 2 Q9BQB8 Q9bqb8 homo sapien  
35 465 25.1 597 2 Q9BU10 Q9bu10 homo sapien  
36 465 25.1 597 2 Q9BB9 Q9bb9 homo sapien  
37 465 25.1 606 2 Q6GMV2 Q6gmv2 homo sapien  
38 465 25.1 613 2 Q8WUX1 Q8wux1 homo sapien  
39 465 25.1 620 2 Q96EY0 Q96ey0 homo sapien  
40 465 25.1 625 2 Q96AA6 Q96aa6 homo sapien  
41 462 24.9 470 2 BAC85387 Bac85387 homo sapi  
42 462 24.9 479 2 AAH14667 AAh14667 homo sapi  
43 460 24.8 391 1 MUCB HUMAN P04220 homo sapien  
44 460 24.8 483 2 BAC85202 Bac85202 homo sapi  
45 459.5 24.8 477 2 BAC85697 Bac85697 homo sapi

## ALIGNMENTS

RESULT 1  
EPC HUMAN STANDARD; PRT; 428 AA.  
ID P01854;  
AC P01854;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE IG epsilon chain C region.  
GN Name=IGHE;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83168897; PubMed=6300763;  
RA Seno M., Kurokawa T., Ono Y., Onda H., Sasaki R., Igarashi K.,  
RA Kikuchi M., Sugino Y., Nishida Y., Honjo I.;  
RT "Molecular cloning and nucleotide sequencing of human immunoglobulin  
epsilon chain cDNA.";  
RL Nucleic Acids Res. 11:719-726(1983).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANT LEU-359.  
RX MEDLINE=83001945; PubMed=6289268;  
RA Max E.B., Battey J., Ney R., Kirsch I.R., Leder P.;  
RT "Duplication and deletion in the human immunoglobulin epsilon genes.";  
RL Cell 29:691-699(1982).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84236029; PubMed=6234164;  
RA Flanagan J.G., Rabbits T.H.;  
RT "The sequence of a human immunoglobulin epsilon heavy chain constant  
region gene, and evidence for three non-allelic genes.";  
RL EMBO J. 1:655-660(1982).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84207910; PubMed=6327276;  
RA Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;  
RT "Long terminal repeat-like elements flank a human immunoglobulin  
epsilon pseudogene that lacks introns.";  
RL EMBO J. 1:1539-1544(1982).  
RN [5]  
RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).  
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RT (In) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
Marcel Dekker, New York (1978).  
RN [6]  
RP SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.  
RX MEDLINE=83065234; PubMed=6815656;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
immunoglobulin epsilon chain expressed in a myeloma cell line.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=87089848; PubMed=3796618;
RA Padlan E.A., Davies D.R.;
RT 'A model of the Fc of immunoglobulin E.';
RL Mol. Immunol. 23:1063-1075(1986).
CC -!- SIMILARITY: Contains 4 immunoglobulin-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L00022; AAB59424.1; ALT_INIT.
DR PIR: A22771; EHHU.
DR PDB: 1F6A; X-ray; B/D=207-428.
DR PDB: 1FP5; X-ray; A=207-428.
DR PDB: 1G84; NMR; A=106-210.
DR PDB: 1IG3; Model; A/B=..
DR PDB: 1OOV; X-ray; A/B=102-428.
DR Genew; HGNC:5522; IGHE.
DR MIM; 147180; ..
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; ig; 4.
DR SMART; SM00407; IGcl; 4.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
DR 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 6 103 IG-like 1.
FT DOMAIN 112 210 IG-like 2.
FT DOMAIN 214 318 IG-like 3.
FT DOMAIN 324 423 IG-like 4.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 15 105 Interchain (with a heavy chain).
FT DISULFID 29 85 Interchain (with a heavy chain).
FT DISULFID 121 121 Interchain (with a heavy chain).
FT DISULFID 135 193 Interchain (with a heavy chain).
FT DISULFID 209 299 N-linked (GlcNAc. . .).
FT DISULFID 239 299 N-linked (GlcNAc. . .).
FT DISULFID 345 405 N-linked (GlcNAc. . .).
FT CARBOHYD 21 21 N-linked (GlcNAc. . .).
FT CARBOHYD 49 49 N-linked (GlcNAc. . .).
FT CARBOHYD 99 99 N-linked (GlcNAc. . .).
FT CARBOHYD 146 146 N-linked (GlcNAc. . .).
FT CARBOHYD 252 252 N-linked (GlcNAc. . .).
FT CARBOHYD 275 275 W -> L (possible polymorphism).
FT VARIANT 359 359 /FTID=VAR_003885.
FT STRAND 113 119;
FT STRAND 130 138;
FT STRAND 148 151;
FT TURN 152 153;
FT STRAND 154 156;
FT HELIX 158 160;
FT STRAND 163 165;
FT STRAND 173 181;
FT HELIX 182 186;
FT TURN 187 188;
FT STRAND 191 196;
FT STRAND 201 206;
FT STRAND 218 221;
FT HELIX 226 230;
FT TURN 231 232;

Query Match 56.0%; Score 1038.5; DB 1; Length 428;
Best Local Similarity 62.4%; Pred. No. 9.3e-72;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

Qy 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVGQEAENLFPYTRPKRG 81
Db 111 PPTVKILQSSCDGGHFPPTIQLCLVSGITPOTINITWLEQGVND--VDLSTATTQE 168
Qy 82 GQTFSLQSEVNIITQGMWSSNTYTCVHGNGSIFEDSRKCADSNPRGSAVLSRSPFD 141
Db 169 GELASTQSELTLSQKEWLSDRYTCQVYQGHFTEDSTKKCADSNPRGSAVLSRSPFD 228
Qy 142 LFRKSPITITCLVVDLAPSGKTNLWSRAGSPVNHSTRKEKQKNGTLTSTLPVGT 201
Db 229 LFRKSPITITCLVVDLAPSGKTNLWSRAGSPVNHSTRKEKQKNGTLTSTLPVGT 288
Qy 202 RDMTEGTYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPETGT--TRTVTCLI 259
Db 289 RDMTEGTYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACLI 347
Qy 260 RGFYPSISVQWMLFNNEEDHTGHTTTRPOKHGTDPSPFLYSRMLVNSIKWKNLVC 319
Db 348 QNFMPEDISVQWLNHEVQLPDARHSTTPRKTGKS--GPEVFSRLLEVTRAENQKDEFFC 405
Qy 320 RVVHEALPGSRITLKSILHVSAG 341
Db 406 RAVHEAASPSQTQVRAVSNVPG 427

RESULT 2
BAC85440 PRELIMINARY; PRT; 571 AA.
ID BAC85440
AC BAC85440;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE CDNA FLJ27315 fis, clone TMS06851, highly similar to Ig epsilon chain
DE C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```



```

RN 11 SEQUENCE FROM N.A.
RP MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RT comparison with the human epsilon gene sequence.";
RL EMBO J. 1:1117-1123 (1982).
RN 12 [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
RN 13 [3]
RP SEQUENCE OF 34-421 FROM N.A.
RX MEDLINE=93117774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain
RT cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856 (1982).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01857; CAA25977.1; -.
DR PIR; A02144; EHMS.
DR HSSP; P01854; IFPS.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003597; Ig cl.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IGH1; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.
FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 By similarity.
FT DISULFID 121 180 By similarity.
FT DISULFID 226 285 By similarity.
FT DISULFID 330 392 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 84 84 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 238 238 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 365 365 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 415 415 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 421 AA; 47320 MW; 5F09BE1F30A06B47 CRC64;
Query Match 40.5%; Score 751; DB 1; Length 421;
Best Local Similarity 44.8%; Pred. NO. 1.3e-49;
Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;
QY 2 FHHHHHTLSPSS-----GPTIIIPYVKLPHSSCDPRGDAHSTIQLLVSGSPAKV 56
Db 73 FTCHVTTPSPFNSRILVRPNVITLPTLELHSSCDPNA-FHSTIQLYCFYGHILNDV 131
QY 57 HVTVLVDGQBAENLFFYTPRPKEGGQTFSLQSEVNITQGMSSNTYCHVKNGSIFE 116
Db 132 SVSWLMDREITDTLAQTVLKEE-GKLASTCKLNITEQQWMSSTFTCKVTSQGVLY 190
QY 117 DSRKCADSNPRGSVAYLSRPSFDLFIKSPITICLVLDLAPSKGTNLTWSRAGRPV 176

```

```

Db 191 AHTERCPDHEPRGVITVLYLPPSLDLYQNGCAPKLTCLVLDSEK-NVNVWQEKTSV 249
QY 177 NHSTRKEEKORNGTLVTSITLPGTRDWIRGEYQCRVTHPHLPRALMRSTTKLPKRLA 236
Db 250 SASQWYTKHNNATTSITSLPVVAKDWIEGYQCIVDHPDFPKPIVRSITITPGQRSA 309
QY 237 PEVYMLPSPPEETGTTRITVTCILIRGFYPSISVQWLFNNEEDHTGHTTTRPKQDGTDP 296
Db 310 PEVYVFPPEESEDKTLTCLIQNFPEPDISVQWLDGDKLINSQHSITTPILKSNQ 369
QY 297 SFFLYSRLVYKSIWEXGNLVTRVVEALPGSRITLKSLSHYSAGN 342
Db 370 GFFIFSRLEVAKTLWTKQFTQVIEHALQKPKLEKTISTSLGN 415

RESULT 5
MUCM_RABIT
ID MUCM_RABIT STANDARD; PRT; 479 AA.
AC P04221;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (A2 ALLOTYPED).
RX MEDLINE=8408930; PubMed=6418803;
RA Bernstein K.B., Alexander C.B., Reddy E.P., Mage R.G.;
RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
RT of VHA2 allotype: comparisons with VHA1 and membrane mu sequences.";
RL J. Immunol. 132:490-495 (1984).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=During differentiation, B lymphocytes switch from
CC expression of isoform Membrane-bound to isoform Secreted;
CC Name=Membrane-bound;
CC IsoId=P04221-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P03988-1; Sequence=External;
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; X01357; AAA31293.1; -.
PIR; A02165; MHRBM.
HSSP; P01861; IADQ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_YHC.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGH1; 2.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
KW Alternative splicing; Glycoprotein; Immunoglobulin C region;
KW Immunoglobulin domain; Transmembrane.
FT NON_TER 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT TRANSMEM 459 476 Potential.
FT DISULFID 14 14 Interchain (with light chain) (Probable).
FT DISULFID 28 90 By similarity.
FT DISULFID 137 200 By similarity.

```



```
FT DISULFID 219 Interchain (with heavy chain) (Probable).
FT DISULFID 249 By similarity.
FT DISULFID 296 Interchain (with heavy chain) (Probable).
FT DISULFID 356 By similarity.
FT CARBOHYD 46 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 114 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 212 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 261 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 277 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 284 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 479 AA; 52351 MW; 689C637A47BE19FC CRC64;

Query Match
Best Local Similarity 26.8%; Score 497.5; DB 1; Length 479;
Matches 11; Conservative 61; Mismatches 153; Indels 25; Gaps 10;

QY 5 HHHTLSLPSGVP-TIIPTVKLPFHSSCDPR---GDAHSTIQLLCLVSGSPAKVHVT 59
DB 94 HNSNRDLRVSPFDSELPNVSVF---IPRDSFGSGTRKSRLLICQATGSPKQISVS 150

QY 60 WLVDGQEAEN---LFPYTPPKREGGQTSLSQSEVNITQGMSSNTYTCVVKHNSIFE 116
DB 151 WLBDGQKVESGLVTKPVEATKAGPATFSISSMLTITSDWLSQSLYTCRDVHRGIFD 210

QY 117 DS---SRKCADSNPRGSAVLSRPPDLPIRKSPITICLVLDLAPSKGTNLTWSRAG 173
DB 211 KNVMSSECTTSPGIVQVPIAPSPADFLSKASRLICLVTDLT-TYSLNISWASHNG 269

QY 174 KPNVHSTRKEEKORNGTLTVSTLTPVGTQRMWIEGTQYQCRVTHPHLPALMRSTTKLPQK 233
DB 270 KALDTHMNITESHFNATFSANGASVCAEDWESGEQFTCTVTHADLPFLKHTISK--SR 327

QY 234 RLA---PEVYMLPPSPPE---TGTRTVTCILRGVFPSEISVQWLENNEEDHTGHHTTTP 288
DB 328 EVAKHPAVVLPFAPREQLVRSATVTCLVKGFSPADVPVQMQQGQLSSDKYVTSAP 387

QY 289 QKDHTGDPSPFLYSRMLVNKSIWEKGNLVTCTRVVHEALP---GSRLEKSLHYSAG 341
DB 388 APEFQAPGLYFTHSTLTVTEEDWNSGETFTCVVVGHEALPHMVTERTVDKSTGEVG 443

RESULT 6
Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match
Best Local Similarity 26.8%; Score 496.5; DB 2; Length 464;
Matches 118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;

QY 35 RGDASTIQLLCLVSGSPAKVHVTW---LVDQEAENLFPYTPRKREGGQTSLSQSE 90
DB 154 RSTSESTVALGCLVKDYPPEVPTVWSNGALTSQ---VHTPPAVL-----QSSGLYSLSV 206

QY 91 VNITQGMSSNTYTCVVKH---NGSIFEDSSRRCADSNP-----RGVSAYLSRSPFP 140
DB 207 VVTSSNF-GTQYTCNVVDHKPSNTKVDKTVKRCCEPCPCAPPVAGSVPLFPKPK 265

QY 141 D-LFIRKSPITICLVLDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTVSTLTPV 199
DB 266 DTLMSRTPETVTCVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREEQFNSIFRVVSVLTV 325

QY 200 GTRDWIEGTQYQCRVTHPHLPALMRSTTKLPGRLAPEVYMLPPSPPE-TGTRTVTC 258
DB 326 VHQDWLNGKEYCKCKVKNKGLPAIEKTIKTKGQRPQVYTLPPSREEMTKNQVSLTCL 385

QY 259 IRGFYPSISVQWLENNEEDHTGHHTTTPRQKDHGTDPSFPFLYSRMLVNKSIWEKGNLVT 318
DB 386 VKGFYPSDIWVESNGQFEN-NYKTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 441

QY 319 CRVHEALPGSRITLEKSLHYSAG 341
DB 442 CSMHEALHNYT-QKSLSLSPG 463

RESULT 7
CAE45931 PRELIMINARY; PRT; 464 AA.
ID CAE45931
AC CAE45931;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN DKFZp686C15213.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match
Best Local Similarity 36.5%; Pred. No. 6.2e-30;
Matches 118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;

QY 35 RGDASTIQLLCLVSGSPAKVHVTW---LVDQEAENLFPYTPRKREGGQTSLSQSE 90
DB 154 RSTSESTVALGCLVKDYPPEVPTVWSNGALTSQ---VHTPPAVL-----QSSGLYSLSV 206

QY 91 VNITQGMSSNTYTCVVKH---NGSIFEDSSRRCADSNP-----RGVSAYLSRSPFP 140
DB 207 VVTSSNF-GTQYTCNVVDHKPSNTKVDKTVKRCCEPCPCAPPVAGSVPLFPKPK 265

QY 141 D-LFIRKSPITICLVLDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTVSTLTPV 199
DB 266 DTLMSRTPETVTCVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREEQFNSIFRVVSVLTV 325

QY 200 GTRDWIEGTQYQCRVTHPHLPALMRSTTKLPGRLAPEVYMLPPSPPE-TGTRTVTC 258
```



```
Db 177 VSNNGALTSQ---VHTFPAVL-----QSSGLYSLSSVTVTPSSNF-GTQYTCNVDPKPS 228
QY 111 NGSTFEDSRKADSNP-----RGVSAYLSRPSPEF-LFIRKSPITICLVVDLAPSKG 162
Db 229 NTKVDKTVRKCCEPCPCAPPVAGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDP 288
QY 163 TVNLTSRASGKPVNHSRKEKQNGTLTVTSLPVGTRDMEGETYQCRVTHPLPRA 222
Db 289 EVQFNWVDGVEVNAKTRFEEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAP 348
QY 223 LMRSTTKLPGRKLAPVYMLPPSPPEE-TGTRTVTCILIRGFYPSFSEISVQWLFNNEEDHTG 281
Db 349 IEKTSIKTKQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN-- 406
QY 282 HHTTRPQKHGTPSPFSLYSRLVKNKSIWEKGNLTVCRVHVALPGSRITLKSILHSYAG 341
Db 407 NYKTPPMLD--SDGSFFLYSKLTVDRSRWQQGNVFCVSYVMEALHNNHYT-QKSLSPG 463

RESULT 10
BAC85483 PRELIMINARY; PRT; 468 AA.
AC BAC85483;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ29011 fis, clone DMC03382, highly similar to Ig gamma-2 chain
DE C region (Human)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermoid tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Hata T., Nakagawa K., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK131045; BAC85483.1;
SQ SEQUENCE 468 AA; 51715 MW; CB3A94413B6C36CA CRC64;

Query Match 26.6%; Score 493.5; DB 2; Length 468;
Best Local Similarity 34.7%; Pred. No. 1.1e-29;
Matches 124; Conservative 66; Mismatches 134; Indels 33; Gaps 13;

QY 5 HHHHTLSLPESG-PVTIIPPTVK---LFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60
Db 124 YYYIGLDVWGQGFVTVSTASTKGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDP 183
QY 61 ----LVDGQAEENLFPYTRPKREGGTFSLQSEVNITQQWMSNTYTCVHXH---NGS 113
Db 184 NSGALTSQ---VHTFPAVL-----QSSGLYSLSSVTVTPSSNF-GTQYTCNVDPKPSNYK 235
QY 114 IFDSSSRKADSNP-----RGVSAYLSRPSPEF-LFIRKSPITICLVVDLAPSKGTN 165
Db 236 VDKTVRKCCEPCPCAPPVAGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVQ 295
QY 166 LTSRASGKPVNHSRKEKQNGTLTVTSLPVGTRDMEGETYQCRVTHPLPRA 225
Db 296 FNNWVDGVEVNAKTRFEEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEK 355
QY 226 STTKLPKRLAPVYMLPPSPPEE-TGTRTVTCILIRGFYPSFSEISVQWLFNNEEDHTGHT 284
Db 356 TISKTKQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN--NYK 413
QY 285 TTRPQKHGTPSPFSLYSRLVKNKSIWEKGNLTVCRVHVALPGSRITLKSILHSYAG 341
Db 414 TTPPMLD--SDGSFFLYSKLTVDRSRWQQGNVFCVSYVMEALHNNHYT-QKSLSPG 467
```

```
RESULT 11
Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC062335; AAH62335.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDDB9348ADC37E6D CRC64;
```

```
Query Match 26.3%; Score 488.5; DB 2; Length 465;
Best Local Similarity 35.0%; Pred. No. 2.6e-29;
Matches 124; Conservative 61; Mismatches 130; Indels 39; Gaps 13;

QY 7 HHTLSLPESGVTIIPPTVK---LFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW--- 60
Db 131 HGTL-----VTSSASTKGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVQFNW 183
QY 61 -LVDGQAEENLFPYTRPKREGGTFSLQSEVNITQQWMSNTYTCVHXH---NGSIFE 116
Db 184 ALTSQ---VHTFPAVL-----QSSGLYSLSSVTVTPSSNF-GTQYTCNVDPKPSNYKDK 235
QY 117 DSSRKADSNP-----RGVSAYLSRPSPEF-LFIRKSPITICLVVDLAPSKGTNLTW 168
Db 236 TVRKCCEPCPCAPPVAGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVQFNW 295
```

236 TVRKKCCVPCPAPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNW 235  
169 SRASGKPVNHSRKEEKQKNGTLTVSTLPVGTEDWIEGETYQCRVTHPHLPALMRSTT 228  
296 YVDGVEVHNAKTPREEQNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPAPIEKTIS 355  
229 KLPGRKLAPVYMLPPSPPEE-TGTTTRTVCLIRGFYPSISVQWLFNNEEDHTGHHTTR 287  
356 KTKGQPREPOVYLLPSPREEMTKNQVSLTCLVKGFYPSDIAVWESNGOPEN--NYNTP 413  
288 PQKHGTDPSFFLYSRMLVKNKSWKGNLTVCRVHEALPGSRTLEKSLHYSAG 341  
414 PMLD--SDGSFFLYSKLTVDKSRWQQGVFSCVMHEALHNYT-QKSLSLSPG 464

Db QY Db QY Db QY  
QY Db QY  
QY Db QY  
Db QY  
Db QY  
Db QY

RESULT 13  
GC2\_HUMAN  
ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig gamma-2 chain C region.  
GN Name=IGHG2;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellison J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy  
chain constant region genes";  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RX TISSUE=Fetal liver;  
RC MEDLINE=843001943; PubMed=6811139;  
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for  
evolution of a gene family";  
RL Cell 29:671-679(1982).  
RN [3]  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RX TISSUE=Fetal liver;  
RC MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
genes";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
evolutionary, and functional implications";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=80001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
domains of a human IgG2 myeloma protein";  
RL Can. J. Biochem. 57:758-767(1979).  
RN [6]  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920;  
RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
immunoglobulin gamma chains";  
RL Mol. Immunol. 16:923-925(1979).

AAH62335  
ID AAH62335 PRELIMINARY; PRT; 465 AA.  
AC AAH62335;  
DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN Hypothetical protein.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Spleen;  
RC MEDLINE=23388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Spleen;  
RC Strausberg R.;  
RI Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC062335; AAH62335.1;  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51325 MW; FDD9B9348AD3736D CRC64;

Query Match 26.3%; Score 488.5; DB 2; Length 465;  
Best Local Similarity 35.0%; Pred. No. 2.6e-29;  
Matches 124; Conservative 61; Mismatches 130; Indels 39; Gaps 13;  
QY 7 HTTSLPESGPTIIPPTVK---LPHSSCDPRGDAHTIOLLCLVSGFSPAKVHTVM--- 60  
DB 131 HGTL-----VTSSASTKGFVPLAPCSRSTSESTAALGCLVKDYFPFPTVSNNG 183

QY 61 -LVDQEAENLFPYTRTPKREGGOTFSLQSEVNITQGMSSNTYTCVHKH---NGSIFE 116  
DB 184 ALTSG---VHTFPAVL---QSSGLYSLSSVTVTPSPNF-GTQTYTCNVDDHKPSNTKVDK 235  
QY 117 DSSRKCADSNP-----RGVSAYLSRPSFDF-LFRKSTTICLVVDLAPSGTGLTW 168

[7]
RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann I., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
[8]
RN SEQUENCE OF 1-121 (DOT).
RN MEDLINE=9525298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin mononuclear
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893 (1995).
[9]
RN DISULFIDE BONDS.
RN MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225 (1971).
[10]
RN DISULFIDE BONDS.
RN MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148 (1969).
[11]
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).
[12]
CC EMBL; J00230; AAB59393.1; -.
CC PIR; A93906; G2HU.
CC HSP; P01857; 100X.
CC Genew; HGNC:5526; IGK2.
CC MM; 147110; -.
CC GO; GO:0005624; C:membrane fraction; NAS.
CC GO; GO:0003823; F:antigen binding; TAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; Ig\_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; IG1; 2.
CC PROSITE; PS00290; IG\_LIKE; 3.
CC PROSITE; PS00290; IG\_MHC; 2.
CC Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83 Interchain (with a heavy chain).
FT DISULFID 102 102 Interchain (with a heavy chain).
FT DISULFID 103 103 Interchain (with a heavy chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 140 200 Interchain (with a heavy chain).
FT DISULFID 246 304
FT SITE 156 156
FT VARIANT 56 60
FT CONFLICT 109 109
SQ SEQUENCE 326 AA; 35884 MW; 831087C6878CF9C CRC64;
AT OR NEAR THE COMPLEMENT-BINDING SITE.
S -> A (in myeloma proteins TIL and ZIE).
C -> S (in Ref. 3).
/ftid=VAR\_003889.
Query Match 26.2%; Score 486.5; DB 1; Length 326;
Best Local Similarity 36.2%; Pred. No. 2.4e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
SQ 35 RGDASTIQLCLVSGFSPAKVHTW----LVDQEAENLFPYTRPKREGGQTFSLQSE 90

Db 16 RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL-----QSSGLYSLSV 68
Qy 91 VNITQGQWMSNTYTCVKH---NGSIPEDSSRKCADSNP-----RGVSAYLSRSPFP 140
Db 69 VTPSSNF-GTQTYTCNVHDHPSNTKVDKTVVERKCCVECPAPPVAGPSVFLFPKPK 127
Qy 141 D-LFTRKSPFTTCLVVDLAPSKGVNLTWSRASKPVNHSRKEKQKQNGTLTIVTSLPV 199
Db 128 DTLMT-SRTPEVTVCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQENFTRVVSULTV 187
Qy 200 GTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGLAPEVYMLPSPPE-TGTRIVTCL 258
Db 198 VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGPREPVYTLPPSREMTKNQVSLTCL 247
Qy 259 IRGTFPSPISVQWLFNNEEDHTGHHTTRPKDHTGTPSPFELYMLVKNKINWKGKGLV 318
Db 248 VKGFYPSDIAVEWESNGOPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQQGNVFS 303
Qy 319 CRVVHEALPGSRTLEKSLHYSAG 341
Db 304 CSVMHEALHNHYT-QKSLSLSPG 325
RESULT 14
Q6N093 PRELIMINARY; PRT; 417 AA.
ID Q6N093;
AC Q6N093;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686i04196 (Fragment).
GN Name=DKFZp686i04196;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI\_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Wambutt R., Haubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640623; CAB45777.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig\_MHC.
DR InterPro; IPR003596; Ig\_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG\_LIKE; 3.
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;
Query Match 26.2%; Score 486.5; DB 2; Length 417;
Best Local Similarity 36.2%; Pred. No. 3.2e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
Qy 35 RGDASTIQLCLVSGFSPAKVHTW----LVDQEAENLFPYTRPKREGGQTFSLQSE 90
Db 107 RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL-----QSSGLYSLSV 159
Qy 91 VNITQGQWMSNTYTCVKH---NGSIPEDSSRKCADSNP-----RGVSAYLSRSPFP 140
Db 160 VTPSSNF-GTQTYTCNVHDHPSNTKVDKTVVERKCCVECPAPPVAGPSVFLFPKPK 218

QY 141 D-LPIKSPITICLVVDLAPSKGTVALTWSRASGKPVNHSRKEEKORNGTLTSTLTPV 199  
Db 219 DTLMSIRTPVTCVVDVSHEDDEVQFNWYDGVVHNAKTPREEQNSTFRVVSVLTV 278  
QY 200 GTRDWIEGETYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPPSPPEE-TGTTRTVTCL 258  
Db 279 VHQDWLNGKEYCKVKNKGLPAPIEKTSIKTKGQPREPQVYTLPPSREEMTKNQVSLTCL 338  
QY 259 IRGFYPSSEISVQWLFNNEEDHTGHTTTRPQDKHGTDPSPFLYSRMLVNKSIWEKGNLVT 318  
Db 339 VKGFYPSDIAVENESNQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 394  
QY 319 CRVVHEALPGSRTLEKSLHYSAG 341  
Db 395 CSVMHEALHNHYT-QKSLSLSPG 416

RESULT 15

CAE45777  
ID CAE45777 PRELIMINARY; PRT; 417 AA.  
AC CAE45777;  
DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
DI 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686I04196 (Fragment).  
GN DKFZP686I04196.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC T-SSUE=Human esophagus tumor;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640823; CAE45777.1; -  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB893C CRC64;

Query Match 26.2%; Score 486.5; DB 2; Length 417;  
Best Local Similarity 36.2%; Pred. No. 3.2e-29;  
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;  
QY 35 RGDHSTIQLCLVSGSPAKVHTW----LVDGQAEANLFPYTRPKREGGOTFSLQSE 90  
Db 107 RSTSESTAALGCLVKDYFPEPTVSNVNSGALTSG--VHTFPAVL---QSSGLYSLSSV 159  
QY 91 VNITQGMSSNTYTCVHKH---NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPF 140  
Db 160 VTVPSSNF-GTQYTCNVNDHKPNKTKVTKVERKCCVECPCPAPPVAGFSVFLFPKPK 218  
QY 141 D-LPIKSPITICLVVDLAPSKGTVALTWSRASGKPVNHSRKEEKORNGTLTSTLTPV 199  
Db 219 DTLMSIRTPVTCVVDVSHEDDEVQFNWYDGVVHNAKTPREEQNSTFRVVSVLTV 278  
QY 200 GTRDWIEGETYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPPSPPEE-TGTTRTVTCL 258  
Db 279 VHQDWLNGKEYCKVKNKGLPAPIEKTSIKTKGQPREPQVYTLPPSREEMTKNQVSLTCL 338  
QY 259 IRGFYPSSEISVQWLFNNEEDHTGHTTTRPQDKHGTDPSPFLYSRMLVNKSIWEKGNLVT 318  
Db 339 VKGFYPSDIAVENESNQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 394  
QY 319 CRVVHEALPGSRTLEKSLHYSAG 341  
Db 395 CSVMHEALHNHYT-QKSLSLSPG 416

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 14:55:18 ; Search time 157 Seconds  
(without alignments)  
781.436 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EPHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	100.0	342	3 AAB06205	Aab06205 Immunogen
2	1786	96.2	338	8 ADF90025	Adf90025 Opossum-h
3	1786	96.2	338	8 ADN00646	Adn00646 OSO prote
4	1786	96.2	347	8 ADF90033	Adf90033 Opossum-h
5	1786	96.2	347	8 ADN00654	Adn00654 OSO-H pro
6	1772	95.5	557	8 ADF90031	Adf90031 Opossum-h
7	1772	95.5	557	8 ADF90035	Adf90035 Opossum-h
8	1772	95.5	557	8 ADN00656	Adn00656 OSO pro
9	1772	95.5	557	8 ADN00652	Adn00652 modOSO
10	1772	95.5	566	8 ADF90029	Adf90029 Opossum-h
11	1772	95.5	566	8 ADF90037	Adf90037 Opossum-h
12	1772	95.5	566	8 ADN00658	Adn00658 OSO-H p
13	1772	95.5	566	8 ADN00650	Adn00650 modOSO
14	1759	94.8	353	8 ADN00661	Adn00661 H-OCO-H p
15	1644.5	88.6	341	3 AAB06208	Aab06208 Immunogen
16	1587.5	85.5	345	3 AAB06207	Aab06207 Immunogen
17	1584.5	85.4	341	3 AAB03644	Aab03644 Opossum I
18	1588.5	84.5	341	3 AAB06206	Aab06206 Immunogen
19	1533.5	82.1	446	6 ADF96587	Adf96587 Opossum I
20	1498.5	80.7	337	8 ADF90022	Adf90022 Opossum-r
21	1498.5	80.7	337	8 ADN00643	Adn00643 ORO prote
22	1486.5	80.1	555	8 ADF90027	Adf90027 Opossum-r
23	1486.5	80.1	555	8 ADN00648	Adn00648 ORORO pro
24	1392.5	75.0	341	3 AAB06202	Aab06202 Immunogen
25	1375	74.1	342	3 AAB06201	Aab06201 Immunogen

26	1285.5	69.3	427	6 ABP96591	Abp96591 Brushtail
27	1045.5	56.3	569	6 AAO19668	Aao19668 GE2 fusio
28	1044	56.2	577	6 ABP96584	Abp96584 Duckbille
29	1038.5	56.0	320	6 AAO19667	Aao19667 Human Ige
30	1038.5	56.0	323	5 AAU80286	Aau80286 Human Ige
31	1038.5	56.0	323	5 AAU80285	Aau80285 Human Ige
32	1038.5	56.0	323	5 AAU80284	Aau80284 Human Ige
33	1038.5	56.0	324	2 AAR83559	Aar83559 Fc(epsilo
34	1038.5	56.0	325	2 AAR75225	Aar75225 Human Ige
35	1038.5	56.0	325	2 AAR77241	Aar77241 Human Ige
36	1038.5	56.0	331	3 AAB03642	Aab03642 Human Ige
37	1038.5	56.0	331	3 ADD25768	Add25768 Binding d
38	1038.5	56.0	367	1 AAF80291	Aaf80291 Interleuk
39	1038.5	56.0	427	6 AAO19666	Aao19666 Human Ige
40	1038.5	56.0	428	5 AAM47863	Aam47863 Human Ige
41	1038.5	56.0	428	5 AAU80283	Aau80283 Human Ige
42	1038.5	56.0	428	5 AAM50340	Aam50340 Human Ige
43	1038.5	56.0	428	6 AAE35113	Aae35113 Human imm
44	1038.5	56.0	428	7 ADD48440	Add48440 Human pro
45	1038.5	56.0	428	7 ADE97382	Ade97382 Human Ige

## ALIGNMENTS

### RESULT 1

AAB06205

ID AAB06205 standard; protein; 342 AA.

XX AC AAB06205;

XX AC AAB06205;

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

XX XX

DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.

XX Human; opossum; immunoglobulin E; Ige; vaccination; infection; allergy;

KW asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.

OS Homo sapiens.

OS Chimeric.

XX WO200025722-A2.

XX 11-MAY-2000.

PF 21-OCT-1999; 99WO-SE001896.

PR 02-NOV-1998; 98US-0106652P.

XX 22-SEP-1999; 99US-00401636.

PA (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum Ige and the heavy chain constant region 3 from the human. It was shown to cause a stronger polyclonal anti-self Ige response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.

XX (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 342 AA;  
 Query Match 100.0%; Score 1856; DB 3; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-146;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPSGPTTIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 DB 1 EFHHHHHTLSLPSGPTTIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
 QY 61 LVDQEAENLFPYTRPKRGQGFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120  
 DB 61 LVDQEAENLFPYTRPKRGQGFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAYLSRSPFDLFIKSPPTICLVLDLAPSKGTNLTWSRAGKPVNHT 180  
 DB 121 KCADSNPRGVSAYLSRSPFDLFIKSPPTICLVLDLAPSKGTNLTWSRAGKPVNHT 180  
 QY 181 RKEKQKNGTLVTSTLPVGTROWISGETYQCRVTHPLPALMRSTTKLPGRLAPEVY 240  
 DB 181 RKEKQKNGTLVTSTLPVGTROWISGETYQCRVTHPLPALMRSTTKLPGRLAPEVY 240  
 QY 241 MLPSPPEETGTRIVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFL 300  
 DB 241 MLPSPPEETGTRIVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFL 300  
 QY 301 YSRMLNKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 YSRMLNKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 2  
 ID ADF90025 standard; protein; 338 AA.  
 XX AC ADF90025;  
 DT 26-FEB-2004 (first entry)  
 DE Opossum-human chimeric IgE polypeptide.  
 XX IG; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;  
 KW antiasthmatic; dermatological.  
 OS Chimeric.  
 OS Didelphis virginiana.  
 OS Homo sapiens.  
 XX WO2003096966-A2.  
 XX 27-NOV-2003.  
 XX 15-MAY-2003; 2003WO-IB002503.  
 XX 21-MAY-2002; 2002US-0382552P.  
 XX (RESI-) RESISTENTIA PHARM AB.  
 XX Lundgren M, Fuentes A, Magnusson A;  
 XX WPI; 2004-042496/04.  
 DR N-PSDB; ADF90024, ADF90023.  
 XX New host cell comprising a nucleic acid vector comprising a  
 PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or  
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE  
 PT polypeptide.  
 XX Claim 3; SEQ ID NO 6; 23pp; English.  
 XX The present sequence is the protein sequence of an opossum CH2-human CH3-  
 CC opussum CH4 (OSO) chimeric IgE polypeptide. A vector comprising DNA  
 CC encoding OSO can be used for recombinant production this chimeric IgE in

CC host, e.g. CHO, cells. The invention provides methods and materials  
 CC related to expressing chimeric IgE proteins. Nucleic acid vectors, host  
 CC cells, and methods for producing chimeric IgE polypeptides are provided.  
 CC When administered to a mammal, the chimeric polypeptides can reduce the  
 CC IGE antibody effects of IGE-related diseases such as asthma, allergies  
 CC and eczema.  
 XX SQ Sequence 338 AA;  
 Query Match 96.2%; Score 1786; DB 8; Length 338;  
 Best Local Similarity 99.4%; Pred. No. 3.6e-140;  
 Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLSPESGPTTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVDDGEAE 68  
 DB 3 TSLSPESGPTTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVDDGEAE 62  
 QY 69 NLFYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128  
 DB 63 NLFYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122  
 QY 129 GVSAYLSRSPFDLFIKSPPTICLVLDLAPSKGTNLTWSRAGKPVNHTSKKQKRN 198  
 DB 123 GVSAYLSRSPFDLFIKSPPTICLVLDLAPSKGTNLTWSRAGKPVNHTSKKQKRN 182  
 QY 189 GTLVTSTLPVGTROWISGETYQCRVTHPLPALMRSTTKLPGRLAPEVYMLPSP 246  
 DB 183 GTLVTSTLPVGTROWISGETYQCRVTHPLPALMRSTTKLPGRLAPEVYMLPSP 242  
 QY 247 BETGTTRVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFLYSRMLV 306  
 DB 243 BETGTTRVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFLYSRMLV 302

RESULT 3  
 ID ADF90025 standard; protein; 338 AA.  
 XX AC ADF90025;  
 DT 17-JUN-2004 (first entry)  
 DE OSO protein, SEQ ID 6.  
 XX Antiallergic; Vaccine; self-IgE; OSO; allergy.  
 XX Synthetic.  
 XX WO2004022094-A1.  
 XX 18-MAR-2004.  
 XX 02-JUN-2003; 2003WO-IB003075.  
 XX 05-SEP-2002; 2002US-0408648P.  
 XX (RESI-) RESISTENTIA PHARM AB.  
 XX Hellman LT, Persson S, Gansson A;  
 XX WPI; 2004-248376/23.  
 DR N-PSDB; ADF900645.  
 XX New composition comprising a self-IgE polypeptide and an aluminum  
 PT compound, useful for inducing an anti self-IgE antibody response in a  
 PT mammal for treating or preventing allergies.  
 XX Claim 3; Fig 8; 102pp; English.



CC The present invention relates to a composition comprising a polypeptide  
 CC and an aluminum compound, where the polypeptide comprises a self-IgE  
 CC polypeptide sequence (e.g., an ORO polypeptide or an OSO polypeptide  
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or  
 CC ADN00661). Administration of the composition to a mammal reduces the  
 CC level of detectable free IgE in the mammal. The composition is useful for  
 CC inducing an anti self-IgE antibody response in a mammal for treating or  
 CC preventing allergies. The present sequence is an OSO protein, used to  
 CC illustrate the invention. The OSO protein contains an opossum CH2 IgE  
 CC domain followed by a human CH3 IgE domain followed by an opossum CH4 IgE  
 CC domain.

XX SQ Sequence 338 AA;

Query Match 96.2%; Score 1786; DB 8; Length 338;  
 Best Local Similarity 99.4%; Pred. No. 3.6e-140;  
 Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDGQAE 68  
 DB 3 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDGQAE 62  
 QY 69 NLFPTTTPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128  
 DB 63 NLFPTTTPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122  
 QY 129 GVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKQORN 188  
 DB 123 GVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKQORN 182  
 QY 189 GTLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKL--PGKRLAPEVYVMLPPSP 246  
 DB 183 GTLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKLAPSPGKRLAPEVYVMLPPSP 242  
 QY 247 EETGTRTIVTCLIRGFYPSISVQWLFNNEEDHTGHHTTTPQKDHGTDPSFFLYSRMLV 306  
 DB 243 EETGTRTIVTCLIRGFYPSISVQWLFNNEEDHTGHHTTTPQKDHGTDPSFFLYSRMLV 302  
 QY 307 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 303 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 4

ADF90033  
 ID ADF90033 standard; protein; 347 AA.

AC ADF90033;

DT 26-FEB-2004 (first entry)

DE Opossum-human chimeric IgE polypeptide.

XX IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;  
 XX antiasthmatic; dermatological.

XX Chimeric.

OS Didelphis virginiana.

OS Homo sapiens.

XX W02003096966-A2.

XX 27-NOV-2003.

XX 15-MAY-2003; 2003WO-IB002503.

XX 21-MAY-2002; 2002US-0382552P.

XX (RESI-) RESISTENTIA PHARM AB.

XX Lundgren M, Fuentes A, Magnusson A;

XX WPI; 2004-042496/04.

DR

DR N-PSDB; ADF90032.

XX New host cell comprising a nucleic acid vector comprising a  
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or  
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE  
 XX polypeptide.

XX Claim 3; SEQ ID NO 14; 23pp; English.

XX The present sequence is the protein sequence of an opossum CH2-human CH3-  
 CC opossum CH4 chimeric IgE polypeptide including a C-terminal polyhistidine  
 CC sequence (OSO-H). A vector comprising DNA encoding OSO-H can be used for  
 CC recombinant production this chimeric IgE in host, e.g. CHO, cells. The  
 CC invention provides methods and materials related to expressing chimeric  
 CC IgE proteins. Nucleic acid vectors, host cells, and methods for producing  
 CC chimeric IgE polypeptides are provided. When administered to a mammal,  
 CC the chimeric polypeptides can reduce the IgE antibody effects of IgE-  
 CC related diseases such as asthma, allergies and eczema.

XX SQ Sequence 347 AA;

Query Match 96.2%; Score 1786; DB 8; Length 347;  
 Best Local Similarity 99.4%; Pred. No. 3.7e-140;

Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDGQAE 68

DB 3 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDGQAE 62

QY 69 NLFPTTTPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128

DB 63 NLFPTTTPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122

QY 129 GVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKQORN 188

DB 123 GVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKQORN 182

QY 189 GTLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKL--PGKRLAPEVYVMLPPSP 246

DB 183 GTLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKLAPSPGKRLAPEVYVMLPPSP 242

QY 247 EETGTRTIVTCLIRGFYPSISVQWLFNNEEDHTGHHTTTPQKDHGTDPSFFLYSRMLV 306

DB 243 EETGTRTIVTCLIRGFYPSISVQWLFNNEEDHTGHHTTTPQKDHGTDPSFFLYSRMLV 302

QY 307 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

DB 303 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 5

ADN00654

ID ADN00654 standard; protein; 347 AA.

XX AC ADN00654;

DT 17-JUN-2004 (first entry)

XX OSO-H protein, SEQ ID 14.

XX Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.

XX Synthetic.

XX W02004022094-A1.

XX 18-MAR-2004.

XX 02-JUN-2003; 2003WO-IB003075.

XX 05-SEP-2002; 2002US-0408648P.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT, Persson S, Gansson A;  
 XX WPI; 2004-248376/23.  
 XX N-PSDB; ADN00653.  
 XX New composition comprising a self-IgE polypeptide and an aluminum  
 PT compound, useful for inducing an anti self-IgE antibody response in a  
 PT mammal for treating or preventing allergies.  
 XX Claim 3; Fig 16; 102pp; English.  
 XX The present invention relates to a composition comprising a polypeptide  
 CC and an aluminum compound, where the polypeptide comprises a self-IgE  
 CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;  
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or  
 CC ADN00661). Administration of the composition to a mammal reduces the  
 CC level of detectable free IgE in the mammal. The composition is useful for  
 CC inducing an anti self-IgE antibody response in a mammal for treating or  
 CC preventing allergies. The present sequence is an OSO protein, used to  
 CC illustrate the invention. The OSO-H protein contains an opossum CH2 IgE  
 CC domain followed by a human CH3 IgE domain followed by an opossum CH4 IgE  
 CC domain. The OSO-H protein also contains a C-terminal polyhistidine tag.  
 XX Sequence 347 AA;  
 SQ

Query Match 96.2%; Score 1785; DB 8; Length 347;  
 Best Local Similarity 99.4%; Pred. No. 3.7e-140;  
 Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
 QY 9 TLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAE 68  
 DB 3 TLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAE 62  
 QY 69 NLPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128  
 DB 63 NLPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122  
 QY 129 GVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLTWASRAGKPVNHSRKEEKQKN 188  
 DB 123 GVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLTWASRAGKPVNHSRKEEKQKN 182  
 QY 189 GTLVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246  
 DB 183 GTLVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 242  
 QY 247 EETGTTTTCILIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLV 306  
 DB 243 EETGTTTTCILIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLV 302  
 QY 307 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 303 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 338  
 RESULT 6  
 ADF90031  
 ID ADF90031 standard; protein; 557 AA.  
 XX AC ADF90031;  
 XX AC ADF90031;  
 XX 26-FEB-2004 (first entry)  
 XX Opossum-human chimeric IgE polypeptide.  
 XX IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;  
 KW antiaethmatic; dermatological; mutant; mutein.  
 XX Chimeric.  
 OS Synthetic.  
 OS Didelphis virginiana.  
 OS Homo sapiens.  
 XX

PN WO2003096966-A2.  
 XX 27-NOV-2003.  
 XX 15-MAY-2003; 2003WO-IB002503.  
 XX 21-MAY-2002; 2002US-0382552P.  
 XX (RESI-) RESISTENTIA PHARM AB.  
 XX Lundgren M, Fuentes A, Magnusson A;  
 XX WPI; 2004-042496/04.  
 XX New host cell comprising a nucleic acid vector comprising a  
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or  
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE  
 PT polypeptide.  
 XX Claim 3; SEQ ID NO 12; 23pp; English.  
 XX The present sequence is the protein sequence of an opossum CH2-human CH3-  
 CC opoosum CH2-human CH3-opoosum CH4 chimeric IgE polypeptide (modOSO).  
 CC The coding sequence for modOSO contains point mutations in the human  
 CC CH3 domains that abolish mast cell receptor binding. A vector comprising  
 CC DNA encoding modOSO can be used for the recombinant production of the  
 CC chimeric IgE in host, e.g. CHO, cells. The invention provides methods and  
 CC materials related to expressing chimeric IgE proteins. Nucleic acid  
 CC vectors, host cells, and methods for producing chimeric IgE polypeptides  
 CC are provided. When administered to a mammal, the chimeric polypeptides  
 CC can reduce the IgE antibody effects of IgE-related diseases such as  
 CC asthma, allergies and eczema.  
 XX Sequence 557 AA;  
 SQ

Query Match 95.5%; Score 1772; DB 8; Length 557;  
 Best Local Similarity 98.5%; Pred. No. 9.9e-139;  
 Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAE 69  
 DB 225 IDIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAE 284  
 QY 70 LFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129  
 DB 285 LFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344  
 QY 130 VSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLTWASRAGKPVNHSRKEEKQKN 189  
 DB 345 VSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLTWASRAGKPVNHSRKEEKQKN 404  
 QY 190 TLTVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPPSP 249  
 DB 405 TLTVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPPSP 464  
 QY 250 GTTTRVTCTLRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLV 309  
 DB 465 GTTTRVTCTLRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLV 524  
 QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557  
 RESULT 7  
 ADF90035  
 ID ADF90035 standard; protein; 557 AA.  
 XX AC ADF90035;  
 XX AC ADF90035;  
 XX 26-FEB-2004 (first entry)  
 XX Opossum-human chimeric IgE polypeptide.  
 DE

XX IGE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;  
 KW antiasthmatic; dermatological.  
 XX Chimeric.  
 OS Digelphis virginiana.  
 OS Homo sapiens.  
 XX WO2003096966-A2.  
 PN 27-NOV-2003.  
 PD 15-MAY-2003; 2003WO-IB002503.  
 XX 21-WAY-2002; 2002US-0382552P.  
 PR (RESI-) RESISTENTIA PHARM AB.  
 PA Lundgren M, Fuentes A, Magnusson A;  
 XX WPI; 2004-042496/04.  
 DR N-PSDB; ADF90034.  
 XX New host cell comprising a nucleic acid vector comprising a  
 PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or  
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IGE  
 PT polypeptide.  
 XX Claim 3; SEQ ID NO 16; 23pp; English.  
 PS The present sequence is the protein sequence of an opossum CH2-human CH3-  
 CC opossum CH2-human CH3-opossum CH4 (OSOSO) chimeric IGE polypeptide. A  
 CC vector comprising DNA encoding OSOSO can be used for recombinant  
 CC production of the chimeric IGE in host, e.g. CHO, cells. The invention  
 CC provides methods and materials related to expressing chimeric IGE  
 CC proteins. Nucleic acid vectors, host cells, and methods for producing  
 CC chimeric IGE polypeptides are provided. When administered to a mammal,  
 CC the chimeric polypeptides can reduce the IGE antibody effects of IGE-  
 CC related diseases such as asthma, allergies and eczema.  
 XX Sequence 557 AA;  
 SQ Query Match 95.5%; Score 1772; DB 8; Length 557;  
 Best Local Similarity 98.5%; Pred. No. 9.9e-139;  
 Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 69  
 Db 225 IDIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 284  
 QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129  
 Db 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344  
 QY 130 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQKNG 189  
 Db 345 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQKNG 404  
 QY 190 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249  
 Db 405 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464  
 QY 250 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 309  
 Db 465 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 524  
 QY 310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 Db 525 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 557  
 RESULT 8  
 ADN00656

ID ADN00656 standard; protein; 557 AA.  
 XX AC ADN00656;  
 XX 17-JUN-2004 (first entry)  
 DT OSOSO protein, SEQ ID 16.  
 DE Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.  
 KW Synthetic.  
 XX WO2004022094-A1.  
 PN 19-MAR-2004.  
 PD 02-JUN-2003; 2003WO-IB003075.  
 XX 05-SEP-2002; 2002US-0408648P.  
 PR (RESI-) RESISTENTIA PHARM AB.  
 PA Hellman LT, Persson S, Gansson A;  
 XX WPI; 2004-248376/23.  
 DR N-PSDB; ADN00655.  
 XX New composition comprising a self-IgE polypeptide and an aluminum  
 PT compound, useful for inducing an anti self-IgE antibody response in a  
 PT mammal for treating or preventing allergies.  
 PS Claim 3; Fig 18; 102pp; English.  
 CC The present invention relates to a composition comprising a polypeptide  
 CC and an aluminum compound, where the polypeptide comprises a self-IgE  
 CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;  
 CC ADN00643, ADN00645, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or  
 CC ADN00661). Administration of the composition to a mammal reduces the  
 CC level of detectable free IgE in the mammal. The composition is useful for  
 CC inducing an anti self-IgE antibody response in a mammal for treating or  
 CC preventing allergies. The present sequence is an OSO protein, used to  
 CC illustrate the invention. The OSOSO protein contains an opossum CH2 IGE  
 CC domain followed by a human CH3 IGE domain followed by an opossum CH2 IGE  
 CC domain followed by a human CH3 IGE domain followed by an opossum CH4 IGE  
 CC domain.  
 XX SQ Sequence 557 AA;  
 Query Match 95.5%; Score 1772; DB 8; Length 557;  
 Best Local Similarity 98.5%; Pred. No. 9.9e-139;  
 Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 69  
 Db 225 IDIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 284  
 QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129  
 Db 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344  
 QY 130 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQKNG 189  
 Db 345 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQKNG 404  
 QY 190 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249  
 Db 405 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464  
 QY 250 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 309  
 Db 465 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 524  
 QY 310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 Db 525 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 557



QY 70 LFPVTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129  
 Db 285 LFPVTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344  
 QY 130 VSAYLSRSPSPDLFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 189  
 Db 345 VSAYLSRSPSPDLFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 404  
 QY 190 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPQKRLAPEVYMLPPSPPEET 249  
 Db 405 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPQKRLAPEVYMLPPSPPEET 464  
 QY 250 GTTRVTCTLRGFPVSEISVQWLFNNEEDHTGHHHTTRPKQKRGDTPSPFFLYSRMLVNKS 309  
 Db 465 GTTRVTCTLRGFPVSEISVQWLFNNEEDHTGHHHTTRPKQKRGDTPSPFFLYSRMLVNKS 524  
 QY 310 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 342  
 Db 525 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 557

## RESULT 11

ADF90037 ID ADF90037 standard; protein; 566 AA.  
 XX AC ADF90037;  
 XX DT 26-FEB-2004 (first entry)  
 XX DE Opossum-human chimeric IgE polypeptide.  
 XX KW IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;  
 XX KW antiasthmatic; dermatological.  
 XX OS Chimeric.  
 OS Synthetic.  
 OS Didelphis virginiana.  
 OS Homo sapiens.  
 XX PN W02003096966-A2.  
 XX PD 27-NOV-2003.  
 XX PF 15-MAY-2003; 2003WO-IB002503.  
 XX PR 21-MAY-2002; 2002US-0382552P.  
 XX PA (RESI-) RESISTENTIA PHARM AB.  
 XX PI Lundgren M, Fuentes A, Magnusson A;  
 XX DR WPI; 2004-042496/04.  
 XX DR N-PSDB; ADF90036.  
 XX PT New host cell comprising a nucleic acid vector comprising a  
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or  
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE  
 PT polypeptide.  
 XX PS Claim 3; SEQ ID NO 18; 23pp; English.  
 XX CC The present sequence is the protein sequence of an opossum CH2-human CH3-  
 CC opoosum CH2-human CH3-opoosum CH4 chimeric IgE polypeptide including a C-  
 CC terminal polyhistidine sequence (OSOSO-H). A vector comprising DNA  
 CC encoding OSOSO-H can be used for recombinant production of OSOSO-H in  
 CC host, e.g. CHO, cells. The invention provides methods and materials  
 CC related to expressing chimeric IgE proteins. Nucleic acid vectors, host  
 CC cells, and methods for producing chimeric IgE polypeptides are provided.  
 CC When administered to a mammal, the chimeric polypeptides can reduce the  
 CC IgE antibody effects of IgE-related diseases such as asthma, allergies  
 CC and eczema.  
 XX SQ Sequence 566 AA;

Query Match 95.5%; Score 1772; DB 8; Length 566;  
 Best Local Similarity 98.5%; Pred. No. 1e-138;  
 Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 10 LSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTVTLVQGEAEN 69  
 Db 225 IDIPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTVTLVQGEAEN 284  
 QY 70 LFPVTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129  
 Db 285 LFPVTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344  
 QY 130 VSAYLSRSPSPDLFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 189  
 Db 345 VSAYLSRSPSPDLFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 404  
 QY 190 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPQKRLAPEVYMLPPSPPEET 249  
 Db 405 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPQKRLAPEVYMLPPSPPEET 464  
 QY 250 GTTRVTCTLRGFPVSEISVQWLFNNEEDHTGHHHTTRPKQKRGDTPSPFFLYSRMLVNKS 309  
 Db 465 GTTRVTCTLRGFPVSEISVQWLFNNEEDHTGHHHTTRPKQKRGDTPSPFFLYSRMLVNKS 524  
 QY 310 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 342  
 Db 525 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 557  
 RESULT 12  
 ADN00658 ID ADN00658 standard; protein; 566 AA.  
 XX AC ADN00658;  
 XX DT 17-JUN-2004 (first entry)  
 XX DE OSOSO-H protein, SEQ ID 18.  
 XX KW Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.  
 XX OS Synthetic.  
 XX PN W02004022094-A1.  
 XX PD 18-MAR-2004.  
 XX PF 02-JUN-2003; 2003WO-IB003075.  
 XX PR 05-SEP-2002; 2002US-0408648P.  
 XX PA (RESI-) RESISTENTIA PHARM AB.  
 XX PI Hellman LT, Persson S, Gansson A;  
 XX DR WPI; 2004-248376/23.  
 XX DR N-PSDB; ADN00657.  
 XX PT New composition comprising a self-IgE polypeptide and an aluminum  
 PT compound, useful for inducing an anti self-IgE antibody response in a  
 PT mammal for treating or preventing allergies.  
 XX PS Claim 3; Fig 20; 102pp; English.  
 XX CC The present invention relates to a composition comprising a polypeptide  
 CC and an aluminum compound, where the polypeptide comprises a self-IgE  
 CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;  
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or  
 CC ADN00661). Administration of the composition to a mammal reduces the  
 CC level of detectable free IgE in the mammal. The composition is useful for  
 CC inducing an anti self-IgE antibody response in a mammal for treating or  
 CC preventing allergies. The present sequence is an OSO protein, used to



PT New composition comprising a self-IgE polypeptide and an aluminum  
 PR compound, useful for inducing an anti self-IgE antibody response in a  
 PR mammal for treating or preventing allergies.

XX Claim 3; Fig 23; 102pp; English.

XX The present invention relates to a composition comprising a polypeptide  
 CC and an aluminum compound, where the polypeptide comprises a self-IgE  
 CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide:  
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or  
 CC ADN00661). Administration of the composition to a mammal reduces the  
 CC level of detectable free IgE in the mammal. The composition is useful for  
 CC inducing an anti self-IgE antibody response in a mammal for treating or  
 CC preventing allergies. The present sequence is H-OCO-H protein, used to  
 CC illustrate the invention. The H-OCO-H protein contains an opossum CH2 IgE  
 CC domain followed by a monkey CH3 IgE domain followed by an opossum CH4 IgE  
 CC domain. The H-OCO-H protein also contains a N- and C-terminal  
 CC polyhistidine tags.

XX Sequence 353 AA;

Query Match 94.8%; Score 1759; DB 8; Length 353;  
 Best Local Similarity 95.3%; Pred. No. 6,7e-138;  
 Matches 328; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60  
 DB 1 EFHHHHHTLSLPESGPTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60  
 QY 61 LVDGQEAENLPPYTRPKREGGQTFSLQSEVNTTQGWMSNTYTCHVKHNGSIFEDSSR 120  
 DB 61 LVDGQEAENLPPYTRPKREGGQTFSLQSEVNTTQGWMSNTYTCHVKHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAYLSRSPDLFRKSPITITCLVVDLAPSKGTVNLTWASGKPVNHST 180  
 DB 121 KCADSNPRGVSAYLSRSPDLFRKSPITITCLVVDLAPSKGTVNLTWASGKPVNHST 180  
 QY 181 RKEEKQKNGTLTSTLPVGTDRDIEGETYQCRVTHPHLPALMRSTTKL--PGKRLAPE 238  
 DB 181 ATGKKQKNGTLTSTLPVGTDRDIEGETYQCRVTHPHLPALMRSTTKL--PGKRLAPE 240  
 QY 239 VYMLPPSPETGTRTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTRPKDHGTDPSF 298  
 DB 241 VYMLPPSPETGTRTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTRPKDHGTDPSF 300  
 QY 299 FLYSRMLVNKSIWEKGNLVCRCVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 FLYSRMLVNKSIWEKGNLVCRCVVHEALPGSRTLEKSLHYSAGN 344

RESULT 15  
 AAB06208  
 ID AAB06208 standard; protein; 341 AA.

XX AC AAB06208;

XX DT 12-SEP-2003 (revised)  
 XX DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.

XX Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
 XX asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.  
 XX Canis sp.  
 XX Chimeric.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SR001896.

XX 02-NOV-1998; 98US-0106652P.  
 PR 22-SEP-1999; 98US-00401636.  
 XX (RESI-) RESISTENTIA PHARM AB.  
 XX PA Hellman LT;  
 XX PI WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of  
 PT immunoglobulin E in mammals.

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy  
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain  
 CC constant region 3 from the dog. It was shown to cause a stronger  
 CC polyclonal anti-self IgE response than peptides consisting of the same  
 CC regions from one mammal. Immunogenic peptides, particularly those  
 CC consisting of different heavy chain constant regions, can be used for  
 CC vaccination in humans, against bacterial and viral infections and  
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.  
 CC (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 341 AA;

Query Match 88.6%; Score 1644.5; DB 3; Length 341;  
 Best Local Similarity 88.0%; Pred. No. 2.2e-128;  
 Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60  
 DB 1 EFHHHHHTLSLPESGPTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60  
 QY 61 LVDGQEAENLPPYTRPKREGGQTFSLQSEVNTTQGWMSNTYTCHVKHNGSIFEDSSR 120  
 DB 61 LVDGQEAENLPPYTRPKREGGQTFSLQSEVNTTQGWMSNTYTCHVKHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAYLSRSPDLFRKSPITITCLVVDLAPSKGTVNLTWASGKPVNHST 180  
 DB 121 KCADSNPRGVSAYLSRSPDLFRKSPITITCLVVDLAPSKGTVNLTWASGKPVNHST 179  
 QY 181 RKEEKQKNGTLTSTLPVGTDRDIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVY 240  
 DB 180 LNKXKDHFGTITVTSTLPVNTNDIEGETYQCRVTHPHLPKDIVRSIAKLPGKRLAPEVY 239  
 QY 241 MLPPSPETGTRTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTRPKDHGTDPSF 300  
 DB 240 MLPPSPETGTRTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTRPKDHGTDPSF 299  
 QY 301 YSRMLVNKSIWEKGNLVCRCVVHEALPGSRTLEKSLHYSAGN 342  
 DB 300 YSRMLVNKSIWEKGNLVCRCVVHEALPGSRTLEKSLHYSAGN 341

Search completed: November 14, 2004, 14:58:12  
 Job time : 167 secs

**This Page Blank (uspto)**



28	407.5	22.0	326	3	US-08-808-720-3	Sequence 3, Appli
29	407.5	22.0	326	4	US-09-467-638-3	Sequence 3, Appli
30	407.5	22.0	328	3	US-08-808-720-1	Sequence 1, Appli
31	407.5	22.0	328	4	US-09-467-638-1	Sequence 1, Appli
32	407.5	22.0	331	3	US-08-808-720-5	Sequence 5, Appli
33	407.5	22.0	331	4	US-09-467-638-5	Sequence 5, Appli
34	406	21.9	309	4	US-09-883-777-7	Sequence 7, Appli
35	405.5	21.8	218	4	US-09-483-588-3	Sequence 3, Appli
36	404.5	21.8	218	4	US-09-483-588-6	Sequence 6, Appli
37	404.5	21.8	247	4	US-09-428-082B-12	Sequence 12, Appl
38	404.5	21.8	269	4	US-09-428-082B-10	Sequence 10, Appl
39	404	21.8	252	4	US-09-428-082B-1066	Sequence 1066, Ap
40	404	21.8	300	4	US-09-883-777-9	Sequence 9, Appli
41	404	21.8	331	3	US-09-178-869-2	Sequence 2, Appli
42	404	21.8	331	4	US-09-761-413-2	Sequence 2, Appli
43	403.5	21.7	248	4	US-09-428-082B-1062	Sequence 1062, Ap
44	403	21.7	281	4	US-09-854-864-10	Sequence 10, Appl
45	402.5	21.7	218	4	US-09-483-588-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-232-539D-56  
; Sequence 56, Application US/08232539D  
; Patent No. 5965709  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardiou, Paula M.  
; TITLE OF INVENTION: Ige Antagonists  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232.539D  
; FILING DATE: 21-Apr-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/178583  
; FILING DATE: 07-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-232-539D-56

Query Match 31.2%; Score 579; DB 2; Length 113;  
Best Local Similarity 98.2%; Pred. No. 1.3e-48;  
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 122 CADSNPRGVSAVLSRPSFDLIRKSPITCLVVDLAPSKGTVALTWSRSGKPVNHSR 161

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: November 14, 2004, 15:03:41 ; Search time 24 Seconds  
(without alignments)  
945.032 Million cell updates/sec  
Title: US-09-401-636-8  
Perfect score: 1856  
Sequence: 1 EPHHHHTLSPESGPVTI.....HEALPGSRLEKSLHYSAQN 342  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 417130

Minimum DB seq length: 0  
Maximum DB seq length: 342

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCUTUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	31.2	113	2	US-08-232-539D-56
2	548.5	29.6	109	3	US-08-466-163B-1
3	548.5	29.6	109	4	US-09-802-096-1
4	548.5	29.6	109	4	US-09-802-077-1
5	538	29.0	106	2	US-08-232-539D-54
6	512	27.6	334	2	US-08-646-981-16
7	508	27.4	119	2	US-08-646-025A-1
8	501.5	27.0	331	2	US-08-646-981-17
9	490.5	26.4	118	3	US-08-466-151-1
10	490	26.4	333	1	US-08-436-463-6
11	490	26.4	333	1	US-08-024-253-6
12	476.5	25.7	329	4	US-09-313-942-12
13	476	25.6	327	2	US-08-761-277A-47
14	475.5	25.6	326	2	US-08-656-586-9
15	457	24.6	330	4	US-09-301-593-22
16	434	23.4	320	2	US-08-579-940-8
17	421.5	22.7	331	3	US-08-808-720-7
18	421.5	22.7	331	3	US-09-467-638-7
19	415.5	22.4	324	2	US-08-579-940-7
20	414	22.3	228	4	US-09-968-362A-27
21	411.5	22.2	218	4	US-09-483-588-7
22	411.5	22.2	229	4	US-09-968-362A-28
23	411.5	22.2	277	4	US-09-428-082B-20
24	411	22.1	253	4	US-09-428-082B-18
25	409	22.0	313	3	US-08-713-558F-36
26	408.5	22.0	217	4	US-09-483-588-5
27	408.5	22.0	283	4	US-09-854-864-9

Db 1 CANSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTR 60  
Qy 182 KEKQKNGTLTVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKLPG 232  
Db 61 KEKQKNGTLTVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSG 111

## RESULT 2

US-08-466-163B-1  
; Sequence 1, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1D1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 1  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-466-163B-1

Query Match 29.6%; Score 548.5; DB 3; Length 109;  
Best Local Similarity 97.2%; Pred. No. 1.1e-45;  
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
Qy 124 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTRKE 183  
Db 1 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTRKE 60  
Qy 184 EKQKNGTLTVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKLPG 232  
Db 61 EKQKNGTLTVTSTLPVGTDRWIEGET-QCRVTHPHLPRALMRSTTKTSG 108

## RESULT 3

US-09-802-096-1  
; Sequence 1, Application US/09802096  
; Patent No. 6685939  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C3US  
; CURRENT APPLICATION NUMBER: US/09/802,096  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 1  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-09-802-096-1

Query Match 29.6%; Score 548.5; DB 4; Length 109;  
Best Local Similarity 97.2%; Pred. No. 1.1e-45;  
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
Qy 124 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTRKE 183  
Db 1 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTRKE 60  
Qy 184 EKQKNGTLTVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKLPG 232  
Db 61 EKQKNGTLTVTSTLPVGTDRWIEGET-QCRVTHPHLPRALMRSTTKTSG 108

## RESULT 4

US-09-802-077-1  
; Sequence 1, Application US/09802077  
; Patent No. 6699472  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C2US  
; CURRENT APPLICATION NUMBER: US/09/802,077  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 1  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-802-077-1

Query Match 29.6%; Score 548.5; DB 4; Length 109;  
Best Local Similarity 97.2%; Pred. No. 1.1e-45;  
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
Qy 124 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTRKE 183  
Db 1 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTRKE 60  
Qy 184 EKQKNGTLTVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKLPG 232  
Db 61 EKQKNGTLTVTSTLPVGTDRWIEGET-QCRVTHPHLPRALMRSTTKTSG 108

## RESULT 5

US-08-232-539D-54  
; Sequence 54, Application US/08232539D  
; Patent No. 5965709  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: IGE Antagonists  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/178583  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-54

Query Match 29.0%; Score 538; DB 2; Length 106;  
Best Local Similarity 98.1%; Pred. No. 1.1e-44;  
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 GVSAYLSRSPDLFTFKSPPTITCLVVDLAPSKGTNLTWSRSGKPVNHSRKKEKORN 188  
DB 1 GVSAYLSRSPDLFTFKSPPTITCLVVDLAPSKGTNLTWSRSGKPVNHSRKKEKORN 60

QY 189 GTLVTSTLPVGRDWEIEGYQCRVTHPHLPRALMRSTTKLPG 232  
DB 61 GTLVTSTLPVGRDWEIEGYQCRVTHPHLPRALMRSTTKTSG 104

RESULT 6  
US-08-646-981-16  
Sequence 16, Application US/08646981  
Patent No. 5852183  
GENERAL INFORMATION:  
APPLICANT: MAEDA, HIROAKI  
APPLICANT: EDA, YASUYUKI  
APPLICANT: KIWACHI, KAZUHIKO  
APPLICANT: ONO, YOICHI  
APPLICANT: TOKIYOSHI, SACHIO  
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE  
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,981  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WEINER, MARC S

US-08-464-025A-1  
Sequence 1, Application US/08464025A  
Patent No. 5994514  
GENERAL INFORMATION:  
APPLICANT: Jardiou et al.  
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,025A  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-464-025A-1

Query Match 27.4%; Score 508; DB 2; Length 119;  
 Best Local Similarity 88.9%; Pred. No. 1.1e-41;  
 Matches 104; Conservative 1; Mismatches 4; Indels 8; Gaps 4;  
 QY 124 DSNPRGVSAYLSRSPD-LFIRKSPITICLVVDLAPSKGTNLTWSRAS---GKPVNHS 179  
 DB 2 DSNPRGVSAYLSRSPD-LFIRKSPITICLVVDLAPSKGTNLTWSRASXXGKPVNHS 61  
 QY 180 TRKEEKOR---NGHLTVSTLPGVTRDWIEGTYQCRVTHPHLPRAL-MRSTTKLPG 232  
 DB 62 TRKEEKORXXXGTLTVSTLPGVTRDWIEGTYQCRVTHPHLPRALXMRSTTKTSG 118

## RESULT 8

US-08-646-981-17  
 ; Sequence 17, Application US/08646981  
 ; Patent No. 5852183  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MAEDA, HIROAKI  
 ; APPLICANT: ED, YASUYUKI  
 ; APPLICANT: KIMACHI, KAZUHIKO  
 ; APPLICANT: ONO, YOICHI  
 ; APPLICANT: TOKIYOSHI, SACHIO  
 ; TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE  
 ; TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE  
 ; TITLE OF INVENTION: IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
 ; STREET: PO BOX 747  
 ; CITY: FALLS CHURCH  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22040-0747  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/646,981  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WEINER, MARC S  
 ; REGISTRATION NUMBER: 32,181  
 ; REFERENCE/DOCKET NUMBER: 1488-106  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 331 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-646-981-17

Query Match 27.0%; Score 501.5; DB 2; Length 331;  
 Best Local Similarity 36.3%; Pred. No. 2.2e-40;  
 Matches 122; Conservative 62; Mismatches 125; Indels 27; Gaps 12;  
 QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSAKVHTWLVGQAEAFPPVTRPKREGG 82  
 DB 5 PSVFPLAPSCG--STSGSTVTLACLVSQYFPEPTVSM-NSGSLTSGVHTFPVSKSG- 60  
 QY 83 QTFSLQSEVNITQGWMSNTVTCVKGNS-----IFDSRRKCADSNP-----RG 129  
 DB 61 -LYLSLSSMVTPESSR-LPSETFTCNVHPATNTKVDKPGVPKSTCKISPCPVPSIGL 118

QY 130 VSAVLSRSPD-LF-IRKSPITICLVVDLAPSKGTNLTWSRASGKPVNHS-TRKEEKOR 187  
 DB 119 PSVFIFPPFKDILIRITPTPEVTCVLDLGREDEVOISWF-VGKEVHTAKTQPRQOF 177  
 QY 188 NGTLTVSTLPGVTRDWIEGTYQCRVTHPHLPRALMRSTTKLPGKSLADEVYMLPSPPE 247  
 DB 178 NSTYRVVSLPIEHQDMLTKGPKRCRVNHHGLPSPPIERTISKARGQAHPQGVVLPSPK 237  
 QY 248 E--TGCTTETVCLIRGVPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSPFLYSRML 305  
 DB 238 ELSGSDVTLCLIKDFPPEIDVWQSNQGPPEFSKYHTTAPOLDE--DGSVFLYSKLS 295  
 QY 306 YNKSWEKGNLVTCTRVVHEALPGSRITLKSILHYSAG 341  
 DB 296 VDKSRWEQDPFTCAVMHEALQNHYT-DLSLSHSPG 330

## RESULT 9

US-08-466-151-1  
 ; Sequence 1, Application US/08466151  
 ; Patent No. 6037453  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jardiou, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Immunoglobulin Variants  
 ; NUMBER OF SEQUENCES: 65  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Winpatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/466,151  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/466163  
 ; FILING DATE: 06-Jun-1995  
 ; APPLICATION NUMBER: 08/405617  
 ; FILING DATE: 15-MAR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/185899  
 ; FILING DATE: 26-JAN-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/879495  
 ; FILING DATE: 07-MAY-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/744768  
 ; FILING DATE: 14-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Svoboda, Craig G.  
 ; REGISTRATION NUMBER: 39,044  
 ; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
 ; TELEPHONE: 650/225-1489  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 118 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; US-08-466-151-1

Query Match 26.4%; Score 490.5; DB 3; Length 118;  
 Best Local Similarity 88.0%; Pred. No. 5.5e-40;  
 Matches 103; Conservative 1; Mismatches 4; Indels 9; Gaps 5;

```

QY 124 DSNPRGVAYLRSPFD-LFIRKPTITCLVVDLAPSKGTNLTWSRAS---GKPVNHS 179
DB 2 DSNPRGVAYLRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRXASXXGKPVNHS 61
QY 180 TRKEERQ---NGTLVTSTLPGVGRDWEGETYQCRVTHPLPRAL-MRSTTKLP 232
DB 62 TRKEERQXXXGTLVTSTLPGVGRDWEGET-QCRVTHPLPRALXWRSTTKTSG 117

RESULT 10
US-08-436-463-6
; Sequence 6, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-6

Query Match 26.4%; Score 490; DB 1; Length 333;
Best Local Similarity 34.2%; Pred. No. 2.9e-39;
Matches 117; Conservative 63; Mismatches 126; Indels 36; Gaps 12;

QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW---LVDGQEAENLPYTRPK 78
DB 4 PSVFPLAPSCOTTSGA--TVALACLVLGYFPFPTVSVNSGALTSG---VHTFPAVL--- 55
QY 79 REGGQTFSLQSEVNITQGMSSNTYTCVVKH--NGSIFEDSSRK-----CADS 125
DB 56 -QASGLYSLSMVTPSSRWL-SDTFCNVAHPSPNTKVDKTRKTDHPGPKPCDCPK 113
QY 126 NP----RGVSAYLRSPFD-LFIRKPTITCLVVDLAPSKGTNLTWSRASGKPVNHS 180
DB 114 PPPEMLGGPSIFIPFPKPTLSISRTPETCLVVDLGGDDSDVQITFWVDNTQVYTA 173
QY 181 RKEEKQRNGTLVTSTLPGVGRDWEGETYQCRVTHPLPRALMRSTTKLPGRKLAPEV 240

```

```

DB 174 SPREQNSYRVVSVLPILHQLKGFCKVNSKSLSPSTERTISKAKGPHEPOVY 233
QY 241 MLPPSPETGTR-TVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTPSPF 299
DB 234 VLPPAQBELSRNKSVTCLIKSFHPDIAVWEITQOPEPENNYRTTTPOLD--SGTYF 291
QY 300 LYSMLVYKSTWKGNIATVCRVHVEALPGSRITKLSLHYSAG 341
DB 292 VYSKLSVDRSHWQGNNTYTCVSHEALHSHHT-QKSLTQSPG 332

RESULT 11
US-08-024-253-6
; Sequence 6, Application US/08024253
; Patent No. 5785968
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; APPLICANT: TOHYA, Yukinobu
; APPLICANT: MIKAMI, Takeshi
; TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
; STREET: 1233 20th Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/024,253
; FILING DATE: 19930301
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 79189/1992
; FILING DATE: 28-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CANTOR, Herbert I.
; REGISTRATION NUMBER: 24,392
; REFERENCE/DOCKET NUMBER: P-500-23744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-0400
; TELEFAX: (202) 835-0605
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-024-253-6

Query Match 26.4%; Score 490; DB 1; Length 333;
Best Local Similarity 34.2%; Pred. No. 2.9e-39;
Matches 117; Conservative 63; Mismatches 126; Indels 36; Gaps 12;

QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW---LVDGQEAENLPYTRPK 78
DB 4 PSVFPLAPSCOTTSGA--TVALACLVLGYFPFPTVSVNSGALTSG---VHTFPAVL--- 55
QY 79 REGGQTFSLQSEVNITQGMSSNTYTCVVKH--NGSIFEDSSRK-----CADS 125
DB 56 -QASGLYSLSMVTPSSRWL-SDTFCNVAHPSPNTKVDKTRKTDHPGPKPCDCPK 113

```

QY 126 NP---RVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHS 180  
DB 114 PPMELGSPSIFIPPKPKTSLSRPEVTCVVDLGDSDVQITWFVDNTQVYAKT 173  
QY 181 RKEKQKNGTLVTVSTLPGVTRDWIEGETYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 240  
DB 174 SPREEQFNSTRVVSUPLHLDWLGKFKCKVNSKSLSPISRTISAKAGPHEPQVY 233  
QY 241 MLPSPBETGTR-TVTCLRGFPVPSISVQWLFNNEEDHTGHTTRPKDGHGTDPSP 299  
DB 234 VLPFAQBELSNKSVTCLIKSFHPPDIAVEWSEITQPEPNRYTTPQLD--SDGTYP 291  
QY 300 LYSRLMYKSWKGNLTVCRVHEALPGSRTLEKSLHYSAG 341  
DB 292 VYSLVDRSHWQGNITYTCSVSEALHSHHT-QKSLTQSPG 332

## RESULT 12

US-09-313-942-12  
; Sequence 12, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-A  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-942-12

Query Match 25.7%; Score 476.5; DB 4; Length 329;  
Best Local Similarity 35.5%; Pred. No. 5.8e-38;  
Matches 122; Conservative 58; Mismatches 131; Indels 33; Gaps 12;  
QY 15 SGVTHIIPVTKLFHSCDPRGDAHSTIQLCLVSGFSPAKVHTW----LVDGQEAENL 70  
DB 1 SGASTKGPSVFPL--APCS-RSTSESTAALGCLVKDYFPEPTVSMNSGALTSG--VHT 54  
QY 71 FVYTRPKREGGQTFSLQSEVNTIQGMSSNTYTCHVKHNGSIFEDSSRKCADSNP--- 127  
DB 55 FPAVL---QSSGLYSLSSVTVFSSS-LGKTYTCNVDRKPSNTKVDKVESKYGPFCP 109  
QY 128 -----RGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWASRSGKPVN 178  
DB 110 SCPAPFLGSPSVFLFPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVNA 169  
QY 179 STRKEKQKNGTLVTVSTLPGVTRDWIEGETYQCRVTHPLPRALMRSTTKLPGRKLAPE 238  
DB 170 KTKPREQFNSTRVVSUPLHLDWLGKFKCKVNSKSLSPISRTISAKAGPHEPQVY 229  
QY 239 VYMLPSPPEE-TGTTTRVTCIRGFYPSISVQWLFNNEEDHTGHTTRPKDGHGTDPSP 297  
DB 230 VYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN--NYKTTTPVLD--SDGS 285  
QY 298 FLYSLMYKSWKGNLTVCRVHEALPGSRTLEKSLHYSAG 341  
DB 286 FFYLSRLTVDKSRWQEGNVFSCVWHEALHNYT-QKSLUSL 328

## RESULT 13

US-08-761-277A-47  
; Sequence 47, Application US/08761277A  
; Patent No. 5972334

; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/761,277A  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/644,664  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: GENITOPB-02406  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 327 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-761-277A-47

Query Match 25.6%; Score 476; DB 2; Length 327;  
Best Local Similarity 35.8%; Pred. No. 6.5e-38;  
Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;  
QY 35 RGDHSTIQLCLVSGFSPAKVHTW----LVDGQEAENLFPYTRPKREGGQTFSLQSE 90  
DB 16 RSTSESTAALGCLVKDYFPEPTVSMNSGALTSG--VHTFPAVL---QSSGLYSLSSV 68  
QY 91 VNTIQGMSSNTYTCHVKHNGSIFEDSSRKCADSNP-----RGVSAYLSRSP 139  
DB 69 VTFPSSS-LGKTYTCNVDRKPSNTKVDKVESKYGPFCPAPFLGSPSVFLFPK 127  
QY 140 FD-LFIRKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHSRKEKQKNGTLVTVSTLP 198  
DB 128 KDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVNAKTPREEQFNSTRVVSU 187  
QY 199 VGRDMEGETYQCRVTHPLPRALMRSTTKLPGRKLAPEVYMLPSPPEE-TGTTTRVTC 257  
DB 188 VLHQDWLNGKEYCKVNSKSLSPISRTISAKAGPHEPQVYTLPPSQEEMTKNQVSLT 247  
QY 258 LIRGFYPSISVQWLFNNEEDHTGHTTRPKDGHGTDPSPFLYSLMYKSWKGNL 317  
DB 248 LVKGFYPSDIAVEWESNGQPEN--NYKTTTPVLD--SDGSFFLYSLTVDKSRWQEGNV 303  
QY 318 TCRVHEALPGSRTLEKSLHYSAG 341  
DB 304 SCVWHEALHNYT-QKSLUSL 326

## RESULT 14

US-08-656-586-9  
; Sequence 9, Application US/08656586  
; Patent No. 5834597  
; GENERAL INFORMATION:

```

; APPLICANT: Tso, J. Yun
; APPLICANT: Cole, Michael S.
; APPLICANT: Anasetti, Claudio
; TITLE OF INVENTION: Mutated No. 593459/activating IgG2 Domains and
; TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,586
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-007210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..326
; OTHER INFORMATION: /note= "heavy chain constant region of
; OTHER INFORMATION: IgG2 mutant 3"
;
; US-08-656-586-9
;
; Query Match 25.6%; Score 475.5; DB 2; Length 326;
; Best Local Similarity 35.8%; Pred. No. 7.2e-38;
; Matches 115; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
;
; QY 35 RGAHSTIQLCLVSGSPAKVHTW---LVDGQEAENLFPYTRPKREGGQTFSLQSE 90
; DB 16 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL---QSSGLYSLSSV 68
;
; QY 91 VNITQGOMMSNTYTCHVKH---NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPF 140
; DB 69 VTPVSSNF-GTQVTVCNVHDKPSNTKVDKTVKCKVCPCPPCPAPPAAAPSVLFPFKPK 127
;
; QY 141 D-LFIRKSPITCLVLDLAPSKGTVALTWSRASKPVNHSSTRKEEQKQNGTLTSTLPV 199
; DB 128 DTLMIPTPEVTCVVVDVSHEDDEVQPNWYVDGVEVHNATKPREEQFNSTFRVSVLV 187
;
; QY 200 GTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGRKLAPVEYMLPPSPPEE-TGTRTVTCL 258
; DB 188 VHQDLNGKEYCKVSKNGLPAPIEKTISKTKGQPREPQVYVTLPPSREEMTKNQVSLTCL 247
;
; QY 259 IRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDTPSPFLYSRLVNSKIWEKGNLVT 318
; DB 248 VKGFYPSDIAVWESNQOPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRQQGVNFS 303
;
; QY 319 CRVVHEALPGSRTLEKSLHS 339
; DB 304 CSNVHEALHNHYT-QKSLSLS 323
;
; RESULT 15
;
; US-09-301-593-22
; Sequence 22, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 22
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-301-593-22
;
; Query Match 24.6%; Score 457; DB 4; Length 330;
; Best Local Similarity 34.7%; Pred. No. 4.6e-36;
; Matches 118; Conservative 56; Mismatches 130; Indels 36; Gaps 12;
;
; QY 22 PPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKVHTW---LVDGQEAENLFPYTRP 77
; DB 6 PSVEFLAPSSKSTSG---GTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL-- 57
;
; QY 78 KREGGQTFSLQSEVNITQGMMSNTYTCHVKNGSIPE-----DSSRKC-----A 123
; DB 58 --QSSGLYSLSSVTVPS--LGTQTYICNVNKKPSNTRKVDKVEPKSCDKHTTCCPCPA 114
;
; QY 124 DSNPRGVSAVLSRPSFPD-LFIRKSPITCLVLDLAPSKGTVALTWSRASKPVNHSSTRK 182
; DB 115 PELIGGPSVFLFPKPKXTLMIPTPEVTCVVVDVSHEDDEVQPNWYVDGVEVHNATK 174
;
; QY 183 EEKQNGTTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGRKLAPVEYML 242
; DB 175 REEQYNSTYRVVSVLTVLHQDLNGKEYCKVSKNGLPAPIEKTISKAKGQPREPQVYVTL 234
;
; QY 243 PPSPEE-TGTRTVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDTPSPFLY 301
; DB 235 PPSREEMTKNQVSLTCLVKGFYPSDIAVWESNQOPEN--NYKTPPVL--SDGSFFLY 290
;
; QY 302 SRMLVNSKIWEKGNLVTCRVVHEALPGSRTLEKSLHSAG 341
; DB 291 SKLTVDKSRQQGVNFSVNVHEALHNHYT-QKSLSLSPG 329
;
; Search completed: November 14, 2004, 15:11:02
; Job time : 25 secs
```

**This Page Blank (uspto)**